

Tue May 18 12:03:01 2004

us-09-730-174a-3.closed.rpr

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:56:10 ; Search time 10.25 Seconds  
(without alignments)  
112.614 Million cell updates/sec

Title: US-09-730-174A-3  
Perfect score: 59  
Sequence: 1 SVSEIQLMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	35.6	12	2	S21205 Ig heavy chain V r
2	18	30.5	7	2	A58718 carcinoin UT49 - Ca
3	18	30.5	9	2	S78420 ribosomal protein
4	18	30.5	10	2	A60589 sperm-activating p
5	18	30.5	10	2	B46453 e antigen p20e pre
6	17	28.8	7	2	I46868 alpha-myosin heavy
7	17	28.8	10	2	S28055 cytochrome b559 co
8	17	28.8	10	2	A37268 Ig heavy chain C r
9	16	27.1	9	2	S13636 coat protein beta
10	16	27.1	10	2	A47364 placental lactogen
11	15	25.4	7	2	S25266 pili protein - Bsc
12	15	25.4	7	2	S29735 polyposphatase-glu
13	15	25.4	9	2	PM0002 chlorophyll a/b-b1
14	15	25.4	9	2	A56029 N-methylpurine DNA
15	15	25.4	10	2	S27873 hypochlorous prote
16	15	25.4	10	2	A38841 rhodopsin homolog
17	15	25.4	11	2	S35490 type II site-speci
18	15	25.4	11	2	B41835 translation elonga
19	15	25.4	11	2	A40795 glycoprotein H-a -
20	15	25.4	12	2	A55837 5-aminimidazole r
21	14	23.7	4	2	I38888 COI intron 16 prot
22	14	23.7	7	2	JN0859 peptidyl-di-peptid
23	14	23.7	7	2	T09512 NADH2 dehydrogenas
24	14	23.7	9	2	PT0238 Ig heavy chain CRD
25	14	23.7	10	2	SPG28K neuropeptide K - pig
26	14	23.7	10	2	C61033 ranatichylinin C -
27	14	23.7	11	2	A55149 tetracenomycin A2
28	14	23.7	11	2	S60354 retinal oxidase -
29	14	23.7	11	2	B29806 acidic proline-rich

30	14	23.7	11	2	PH0904 T-cell receptor be
31	14	23.7	11	2	PH0924 T-cell receptor be
32	14	23.7	11	4	S41909 hypothetical prote
33	14	23.7	12	2	S25485 transcription fact
34	14	23.7	12	2	G49410 t-complex polypept
35	14	23.7	12	2	S71034 porB protein - Sal
36	14	23.7	12	2	C60529 hemocyanin I - gre
37	14	23.7	12	2	PH1190 T-cell receptor al
38	14	23.7	12	2	PH1187 T-cell receptor al
39	14	23.7	12	2	PH1189 T-cell receptor al
40	14	23.7	12	2	I41235 glutamine-tRNA lig
41	13	22.0	6	2	A20186 fatty-acid synthas
42	13	22.0	8	2	T14906 hypothetical prote
43	13	22.0	8	2	JS0316 leucokinin VI - Ma
44	13	22.0	8	2	PH1618 Ig H chain V-D-U r
45	13	22.0	9	2	JN0026 sperm-activating p

## ALIGNMENTS

### RESULT 1

S21205  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C/Accession: S21205  
R/Makiya, R./ Stigbrand, T.  
Eur. J. Biochem. 205, 341-345, 1992  
A/Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin-  
A/Reference number: S21205; PMID:92209522; PMID:1555592  
A/Accession: S21205  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12 <MAK>  
C/Keywords: heterotetramer; immunoglobulin

Query Match 35.6% ; Score 21; DB 2; Length 12;  
Best Local Similarity 44.4% ; Pred. No. 6.5e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 EIQLMHNLG 12  
DB 1 EVQLVESGG 9

RESULT 2  
A58718  
Carnocin UT49 - Carnobacterium sp. (fragment)  
C/Species: Carnobacterium sp.  
C/Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998  
C/Accession: A58718  
R/Stoefels, G./ Missen-Ney, J./ Gudmundsdottir, A./ Sletten, K./ Hojo, H./ Nes, I.F.  
Appl. Environ. Microbiol. 58, 1417-1422, 1992  
A/Title: Purification and characterization of a new bacteriocin isolated from a Carnobac  
A/Reference number: A58718; PMID:92321768; PMID:1622206  
A/Accession: A58718  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <STO>  
C/Keywords: antibiotic; lanthionine

Query Match 30.8% ; Score 18; DB 2; Length 7;  
Best Local Similarity 100.0% ; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6  
DB 2 SEIQ 5

RESULT 3  
S78420

ribosomal protein RL41, mitochondrial [validated] - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)  
C/Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000  
C/Accession: S78420  
R/Goldschmidt-Reisin, S.; Grack, H.R.  
submitted to the Protein Sequence Database, February 1998  
A/Reference number: S78411  
A/Accession: S78420  
A/Molecule type: protein  
A/Residues: 1-9 <GOL>  
A/Note: the protein is designated as mitochondrial ribosomal protein L41  
C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 30.5%; Score 18; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12  
DB 5 HRLG 8

RESULT 4  
A60589  
sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchin  
C/Species: Heterocentrotus mammillatus  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
C/Accession: A60589  
R/Toshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi, K.  
Comp. Biochem. Physiol. B 94, 739-751, 1989  
A/Title: A halogenated amino acid-containing sperm activating peptide and its related peptides  
A/Reference number: A60527  
A/Accession: A60589  
A/Molecule type: protein  
A/Residues: 1-10 <TOS>  
C/Superfamily: unassigned animal peptides

Query Match 30.5%; Score 18; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 2e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNLG 12  
DB 2 YNLG 5

RESULT 5  
B46453  
e antigen p20e precursor - hepatitis B virus (subtype adr) (fragment)  
N/Alternate names: HBe antigen precursor  
N/Contains: e antigen  
C/Species: hepatitis B virus, HBV  
A/Variety: subtype adr  
C/Date: 18-Jun-1993 #sequence\_revision 08-Nov-1996 #text\_change 15-Aug-1997  
C/Accession: B46453  
R/Takanaishi, K.; Kishimoto, S.; Ohori, K.; Yoshitawa, H.; Machida, A.; Ohnuma, H.; Tsuda, J. Immunol. 147, 3156-3160, 1991  
A/Title: Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepa  
A/Reference number: A46453; MUID:92013147; PMID:1717588  
A/Accession: B46453  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <TRX>  
A/Experimental source: subtype adr  
A/Note: sequence extracted from NCBI backbone (NCBIP:60243)  
F/1-10/Domain: signal sequence (fragment) #status predicted <SIG>

Query Match 30.5%; Score 18; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 IQLMH 9

DB 1 MOLFH 5

RESULT 6  
146868  
alpha-myosin heavy chain - rabbit (fragment)  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 05-Nov-1999  
C/Accession: 146868  
R/Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.  
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984  
A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula  
A/Reference number: 146868; MUID:84221901; PMID:6328491  
A/Accession: 146868  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-7 <FRI>  
A/Cross-references: GB:K01698; NID:G165538; PID:AAA31415.1; PID:G165539

Query Match 28.8%; Score 17; DB 2; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QLMHN 10  
DB 1 QKMD 5

RESULT 7  
S28055  
cytochrome b559 component psbf - pepper chloroplast (fragment)  
C/Species: chloroplast Capsicum annuum (pepper)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-Jun-1999  
C/Accession: S28055  
R/Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.  
Plant Mol. Biol. 20, 1185-1186, 1992  
A/Title: The psbf gene from bell pepper (Capsicum annuum): plastid RNA editing also occur  
A/Reference number: S28055; MUID:93099270; PMID:1463853  
A/Accession: S28055  
A/Molecule type: DNA  
A/Residues: 1-10 <KUN>  
A/Cross-references: EMBL:X65570; NID:G14344; PID:CAA46539.1; PID:G145724  
C/Genetics:  
A/Gene: psbf  
A/Genome: chloroplast  
C/Superfamily: cytochrome b559 component F  
C/Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match 28.8%; Score 17; DB 2; Length 10;  
Best Local Similarity 37.5%; Pred. No. 3.1e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIOLM 8  
DB 1 SISAMQFI 8

RESULT 8  
A37268  
19 heavy chain C region (129) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998  
C/Accession: A37268  
R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6607-6613, 1991  
A/Title: Heavy and light chain variable region sequences and antibody properties of anti  
A/Reference number: A38740; MUID:91177923; PMID:1706720  
A/Accession: A37268  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-10 <RUP>

Query Match 28.8%; Score 17; DB 2; Length 10;  
Best Local Similarity 44.4%; Pred. No. 3.1e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQMHNIG 12  
| | | | |  
Db 1 ESQSPFNVG 9

RESULT 9  
S13636  
coat protein beta chain, Golgi-derived - rabbit (fragment)  
N/Alternate names: beta-COP protein  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
C/Accession: S13636  
R/Seifried, T.; Stenbeck, G.; Brecht, A.; Lottspeich, F.; Orci, L.; Rothman, J.E.; Wieda  
Nature 349, 215-220, 1991  
A/Title: A coat subunit of Golgi-derived non-clathrin-coated vesicles with homology to t  
A/Reference number: S13636; PMID:91101693; PMID:1898984  
A/Accession: S13636  
A/Molecule type: protein  
A/Residues: 1-9 <SER>  
A/Superfamily: coatomer complex beta chain  
C/Keywords: Golgi apparatus; protein transport

Query Match 27.1%; Score 16; DB 2; Length 9;  
Best Local Similarity 37.5%; Pred. No. 2.8e+05;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIQLM 8  
| | | | |  
Db 1 STGEIPIV 8

RESULT 10  
A47364  
placental lactogen-I precursor - mouse (fragment)  
C/Species: Mus sp. (mouse)  
C/Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
C/Accession: A47364  
R/Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.  
Mol. Endocrinol. 7, 181-188, 1993  
A/Title: Trophectoderm-specific transcription from the mouse placental lactogen-I gene pro  
A/Reference number: A47364; PMID:9325959; PMID:8469232  
A/Accession: A47364  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-10 <RES>  
A/Cross-references: GB:S58124; NID:G299449

Query Match 27.1%; Score 16; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 4.9e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IQLMNL 11  
| | | | |  
Db 1 MQTLNL 7

RESULT 11  
S25266  
p1E protein - Escherichia coli (fragment)  
C/Species: Escherichia coli  
C/Date: 28-May-1993 #sequence\_revision 28-May-1993 #text\_change 11-Jun-1993  
C/Accession: S25266  
R/Dupuy, B.; Tah, M.K.; Posot, O.; Marchal, C.; Pugsley, A.P.  
Mol. Microbiol. 6, 1887-1894, 1992  
A/Title: P1E, a component of the pullulanase secretion pathway of Klebsiella oxytoca, c  
A/Reference number: S25266; PMID:92374839; PMID:1354833  
A/Accession: S25266  
A/Molecule type: protein  
A/Residues: 1-7 <DUP>

C/Genetics:  
A/Genes: p1E

Query Match 25.4%; Score 15; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQLM 8  
| | | | |  
Db 4 IEIM 7

RESULT 12  
S29735  
polyphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenreichi  
C/Species: Propionibacterium freudenreichi subsp. shermanii  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 03-Jun-2002  
C/Accession: S29735  
R/Phillips, N.F.B.; Horn, P.J.; Wood, H.G.  
Arch. Biochem. Biophys. 300, 309-319, 1993  
A/Title: The polyphosphate and ATP-dependent glucokinase from Propionibacterium sherman  
A/Reference number: S29735; PMID:93143332; PMID:8380966  
A/Accession: S29735  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <PHI>  
C/Keywords: phosphotransferase

Query Match 25.4%; Score 15; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12  
| | | | |  
Db 2 HVLG 5

RESULT 13  
PW0002  
chlorophyll a/b-binding protein 31k - green alga (Dunaliella tertiolecta) (fragment)  
N/Alternate names: photosystem II light-harvesting chlorophyll 31k protein  
C/Species: Dunaliella tertiolecta  
C/Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 24-Nov-1999  
C/Accession: PW0002  
R/Laroche, J.; Bennett, J.; Falkowski, P.G.  
Gene 95, 165-171, 1990  
A/Title: Characterization of a cDNA encoding for the 28.5-kDa LHClI apoprotein from the  
A/Reference number: UW0040; PMID:9105528; PMID:2249775  
A/Accession: PW0002  
A/Molecule type: protein  
A/Residues: 1-9 <LAR>  
A/Superfamily: chlorophyll a/b-binding protein  
C/Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane pr

Query Match 25.4%; Score 15; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 EIQLM 8  
| | | | |  
Db 5 EMQAM 9

RESULT 14  
A56029  
N-methylpurine DNA glycosylase - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 19-Jan-1996  
C/Accession: A56029  
R/Roy, R.; Brooks, C.; Mitra, S.  
Biochemistry 33, 15131-15140, 1994  
A/Title: Purification and biochemical characterization of recombinant N-methylpurine-DNA  
A/Reference number: A56029; PMID:95092772; PMID:7999773

Tue May 18 12:03:01 2004

us-09-730-174a-3.closed.rpr

Page 4

A/Accession: A56029  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <ROY>

Query Match 25.4%; Score 15; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12  
|||  
Db 3 HEVG 6

RESULT 15

S27873  
hypothetical protein 2 LRH-1 5'-region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
C/Accession: S27873  
R/Tugwood, J.D.; Isseman, I.; Green, S.  
submitted to the EMBL Data Library, February 1992  
A/Description: LRH-1: A nuclear hormone receptor active in the absence of exogenous ligand  
A/Reference number: S27873  
A/Accession: S27873  
A/Molecule type: mRNA  
A/Residues: 1-10 <TUG>  
A/Cross-references: EMBL:M81385; NID:G198872; PIDN:AAA39446.1; PID:G198874  
C/Superfamily: unassigned leader peptides

Query Match 25.4%; Score 15; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 7.6e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQ 6  
|||  
Db 5 NLSTIQ 10

Search completed: May 18, 2004, 10:05:40  
Job time : 11.25 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:43:45 ; Search time 6.75 Seconds

(without alignments)  
92.569 Million cell updates/sec

Title: US-09-730-174A-3  
Perfect score: 59  
Sequence: 1 SVSEIQLMHNIG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	18	30.5	7	1	LANC CARUI
2	17	28.8	10	1	PSBF CAPAN
3	16	27.1	8	1	ALB6 CYDO
4	16	27.1	8	1	FUSS FUSCO
5	16	27.1	10	1	RRLP PHOIV
6	15	25.4	11	1	ERG CLOPA
7	15	25.4	11	1	PVKI PERAM
8	15	25.4	11	1	TRP1 PROIV
9	14	23.7	7	1	TRP1 PSERU
10	14	23.7	7	1	ALB7 CYDO
11	14	23.7	8	1	ALB8 CARMA
12	14	23.7	8	1	ALB1 CYDO
13	14	23.7	9	1	FAR8 MACRS
14	14	23.7	9	1	UF02 MOUSE
15	14	23.7	10	1	ALB9 CARMA
16	14	23.7	10	1	TRNK RANTR
17	14	23.7	10	1	TRNK RANTR
18	14	23.7	10	1	TRNK PIG
19	14	23.7	11	1	ASU1 BACSE
20	14	23.7	12	1	CDI4 LITXA
21	14	23.7	12	1	CDI4 LITXA
22	14	23.7	12	1	HCY1 CARMA
23	14	23.7	12	1	FOR1 METTM
24	14	23.7	12	1	RS19 TOBEP
25	13	22.0	8	1	LCR6 LEUMA
26	13	22.0	8	1	LCR6 LEUMA
27	13	22.0	9	1	MOSH CLUYA
28	13	22.0	9	1	PSK1 PERAM
29	13	22.0	11	1	CS15 BACSU
30	13	22.0	11	1	OZ0A COMTE
31	13	22.0	12	1	PA2B VIPRO
32	13	22.0	12	1	PKR4 PERU
33	13	22.0	12	1	UR2 POLSP

34	12	20.3	9	1	FIBB PAPHA	P19343 papio hamad
35	12	20.3	9	1	RE42 LITRU	P82075 litoria rub
36	12	20.3	10	1	GLEW HUMAN	P02728 homo sapien
37	12	20.3	10	1	GONI CLUPA	P81749 clupea pall
38	12	20.3	10	1	GON2 CHEPR	P80678 cheilosoma
39	12	20.3	10	1	HTP1 ROMMT	P18110 romalea mic
40	12	20.3	10	1	HTF HEIZE	P16353 heliothis z
41	12	20.3	10	1	SYK CAMUP	Q46464 campylobact
42	12	20.3	10	1	TKNB RANRI	P29135 rana ridibu
43	12	20.3	11	1	CSX1 CONMR	P58807 conus marmo
44	12	20.3	11	1	HS70 PINPS	P81672 pinus pins
45	12	20.3	12	1	HEP1 BACSE	P83054 bacteroides

## ALIGNMENTS

RESULT 1  
ID LANC CARUI STANDARD; PRT; 7 AA.  
AC P36960;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lantibiotic carnocin U149 (Fragment).  
OS Carnobacterium sp. (strain U149).  
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
OC Carnobacterium.  
OX NCBI\_TaxID=35782;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=22321768; PubMed=1622206;  
RA Stoffels G., Nissen-Weyer J., Gudmundsdottir A., Sletten K., Holo H.,  
RA Nes I.F.,  
RT "Purification and characterization of a new bacteriocin isolated from  
a Carnobacterium sp.",  
RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
CC -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).  
KW Active on Gram-positive bacteria.  
KM Antibiotic; Bacteriocin; Lantibiotic.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 30.5%; Score 18; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEQ 6  
DB 2 SEQ 5

## RESULT 2

ID PSBF CAPAN STANDARD; PRT; 10 AA.  
AC Q03367;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI)  
DE (Fragment).  
OS PSBF.  
OS Capsicum annuum (Bell pepper).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Capsicum.  
OX NCBI\_TaxID=4072;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Lamuyo; TISSUE=Frutic, and Leaf;  
RX MEDLINE=93099270; PubMed=1463853;  
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;

RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA  
 RT editing also occurs in non-photosynthetic chromoplasts.";  
 RL Plant Mol. Biol. 20:1185-1188(1992).  
 CC -1- FUNCTION: This b-type cytochrome is tightly associated with the  
 CC reaction center of photosystem II and possibly is part of the  
 CC water-oxidation complex.  
 CC -1- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.  
 CC -1- SIMILARITY: Belongs to the psbD / psbF family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X65570; CAA46539.1; -  
 CC PIR: S28055; S28055.  
 DR HAMAP: MF\_00643; -; 1.  
 DR InterPro: IPR006216; GYC\_B559.  
 DR PROSITE: PS00537; CYTOCHROME\_B559; PARTIAL.  
 KW Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.  
 FT NON TER 1 1  
 FT TRANSMEM <1 5  
 FT DOMAIN 6 10 BY SIMILARITY.  
 FT SEQUENCE 10 AA; 1180 MW; 817D0F59D6D5DC5 CRC64;  
 LUMENAL (POTENTIAL).  
 Query Match 28.8%; Score 17; DB 1; Length 10;  
 Best Local Similarity 37.5%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIQLM 8  
 Db 1 SISAMQFI 8  
 RESULT 3  
 AL16 CYDPO STANDARD; PRT; 8 AA.  
 ID AL16 CYDPO STANDARD; PRT; 8 AA.  
 AC P62157;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 6.  
 OS Cydia pomonella (codling moth).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 CC NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RL "Lepidopteran peptides of the allostatin superfamily.";  
 RT Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: Belongs to the allostatin family.  
 CC KM Neuropeptide; Amidation.  
 FT MOD RES 8  
 FT SEQUENCE 8 AA; 936 MW; 0B2879C45B73767 CRC64;  
 AMIDATION.  
 Query Match 27.1%; Score 16; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MENTLG 12  
 Db 3 LYNFG 7

RESULT 4

FUSO FUSO STANDARD; PRT; 8 AA.  
 ID FUSO FUSO STANDARD; PRT; 8 AA.  
 AC P61010;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Allergen Fus s. I3596\* (Fragment).  
 OS Ficus solani (subsp. pisi) (Nectria haematococca).  
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 CC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
 CC NCBI\_TaxID=70791;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=LARI 3596; TISSUE=Mycelium;  
 RA Verma J., Gangai S.V.;  
 RL Submitted (JUL-1997) to Swiss-Prot.  
 CC -1- ALLERGEN: Causes an allergic reaction in human.  
 KW Allergen.  
 FT NON TER 8  
 FT SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;  
 Query Match 27.1%; Score 16; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMENL 11  
 Db 3 MSHNV 7

RESULT 5  
 RRPL PRODV STANDARD; PRT; 10 AA.  
 ID RRPL PRODV STANDARD; PRT; 10 AA.  
 AC P35916;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE RNA polymerase beta subunit (EC 2.7.7.48) (large structural protein)  
 DE (L protein) (Fragment).  
 GN L.  
 OS Phocine distemper virus (PDV).  
 CC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 CC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
 CC NCBI\_TaxID=11240;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Juster/88;  
 RX MEDLINE=92266877; PubMed=1568321;  
 RA Curran M.D., O'Loon D., Kennedy S., Rima B.K.;  
 RA "Molecular characterization of phocine distemper virus: gene order  
 RT and sequence of the gene encoding the attachment (H) protein.";  
 RL J. Gen. Virol. 73:1189-1194(1992).  
 CC -1- FUNCTION: Probable component of the active polymerase. It may  
 CC function in mRNA synthesis, capping, methylation and poly(A)  
 CC synthesis of newly synthesized viral mRNAs. RNA editing of the P  
 CC gene transcript, and protein kinase activity.  
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
 CC (RNA) (N).  
 CC -1- SIMILARITY: Belongs to the paramyxoviruses L protein family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: D10371; BAA01208.1; -  
 DR Transferase; RNA-directed RNA polymerase.  
 FT NON TER 10 10  
 FT SEQUENCE 10 AA; 1105 MW; 9C2B7FDA52D5A2D5 CRC64;

```

Query Match      27.1%; Score 16; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 SVSEIQLM 8
      ||| |||
      3 SVSVNQIL 10

Db

RESULT 6
EFG_CLOPA
AC P81350; STANDARD; PRT; 11 AA.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OK NCBI_TaxID=1501;
RN (1)
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Pfleger R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of
the nascent protein chain from the A-site to the P-site of the
ribosome.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACITOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON TER 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C3B17 CRC64;

QY      5 IOLMENIG 12
      ||| |||
      4 LEKFORIG 11

Db

Query Match      27.1%; Score 16; DB 1; Length 11;
Best Local Similarity 25.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 SVSEIQLM 8
      ||| |||
      3 SVSVNQIL 10

Db

RESULT 7
PVK1_PERAM
ID PVK1_PERAM STANDARD; PRT; 11 AA.
AC P41837;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-1 (Pee-PVK-1).
OS Periplaneta americana (American cockroach).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OK NCBI_TaxID=6978;
RN (1)
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=95232021; PubMed=7716075;
RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT "Periviscerokinin (Pee-PVK): a novel myotropic neuropeptide from the
perisymphathetic organs of the American cockroach."
RT Peptides 16:61-66(1995).
CC -1- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE

```

```

CC      HYPERNEURAL MUSCLE.
KW Neuropeptide; Amidation.
FT MOD RES 11
SQ SEQUENCE 11 AA; 1114 MW; 39DE5419D7605728 CRC64;

QY      1 SVSEIQLM 8
      ||| |||
      3 SVSVNQIL 10

Db

Query Match      25.4%; Score 15; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      5 IOLMENIG 10
      ||| |||
      6 IPVFRN 11

Db

RESULT 8
T2P1_PROVU
ID T2P1_PROVU STANDARD; PRT; 11 AA.
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Type II restriction enzyme PvuII (EC 3.1.21.4) (Endonuclease PvuII
(R.PvuII) (Fragment).
GN PVUIR.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OK NCBI_TaxID=585;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13315;
RX MEDLINE=93087186; PubMed=1454536;
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvuII restriction and
RT modification system."
RL Nucleic Acids Res. 20:5743-5747(1992).
CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CLEAVES AFTER T-4.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
specific double-stranded fragments with terminal 5'-phosphates.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L04163; AAA25660.1; -
DR PIR; S35490; S35490.
DR REBASE; 1541; Pvui.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
FT NON TER 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

QY      1 SVSEIQLM 8
      ||| |||
      3 SVSVNQIL 10

Db

Query Match      25.4%; Score 15; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 SVSEIQLM 8
      ||| |||
      3 SVSVNQIL 10

Db

RESULT 9
TRP1_PSEPU
ID TRP1_PSEPU STANDARD; PRT; 6 AA.
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE HTH-type transcriptional regulator trp1 (trpA operon transcriptional

```

DE activator) (Fragment).  
 GN TRPI.  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PGI C18;  
 RX MEDLINE=8935826; PubMed=2503057;  
 RA Eberly L., Crawford I.P.;  
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas putida";  
 RL Biochimie 71:521-531(1989).  
 CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE TRPA OPERON, OVERLAPPING ITS OWN PROMOTER REGION.  
 CC -1- SIMILARITY: Contains 1 HTH LysR-type DNA-binding domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by, and for commercial entities requires a license agreement (See <http://www.isb-sdb.ch/announce/> or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC -----  
 DR EMBL; X13299; CAA31660.1; -  
 DR InterPro; IPR000847; HTH\_LYER.  
 DR PROSITE; PS00931; HTH\_LYER; PARTIAL.  
 KM Tryptophan biosynthesis; Transcription regulation; Activator;  
 KM DNA-binding.  
 FT MOD\_RBS 6  
 FT NON\_TER 6  
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F00 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 6;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 LHMNL 11  
 : : :  
 Db 1 MAHDL 5

RESULT 10  
 ALL7\_CYPDPO STANDARD; PRT; 7 AA.  
 ID ALL7\_CYPDPO  
 AC P82158;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 7  
 OS Cydia pomonella (Coddling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 CC  
 KM Neuropeptide; Amidation.  
 FT MOD\_RBS 7  
 FT SEQUENCE 7 AA; 873 MW; 672879CAB8569350 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 7;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 MNLG 12  
 : : :  
 Db 2 MYDFG 6

RESULT 11  
 AL18\_CARMA STANDARD; PRT; 8 AA.  
 ID AL18\_CARMA  
 AC P81821;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinus maenas 18.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=9812193; PubMed=9461295;  
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the RT allatostatin superfamily in the shore crab Carcinus maenas".  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 KM Neuropeptide; Amidation; Multigene family (POTENTIAL).  
 FT MOD\_RBS 8  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 919 MW; C82879D5AB569AB5 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MNLG 12  
 : : :  
 Db 3 MYDFG 7

RESULT 12  
 ALL1\_CYPDPO STANDARD; PRT; 8 AA.  
 ID ALL1\_CYPDPO  
 AC P82152;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 1.  
 OS Cydia pomonella (Coddling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 CC  
 KM Neuropeptide; Amidation.  
 FT MOD\_RBS 8  
 FT SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 HN LG 12  
 Db 4 YNFG 7

## RESULT 13

FAR8\_MACRS

ID FAR8\_MACRS STANDARD; PRT; 9 AA.

AC P83281;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide F8P8 (VSHNNFLRF-amide).  
 OS Macrobryachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonidae; Palaemonidae; Macrobryachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Dysenteric;  
 RX MEDLINE=21107394; PubMed=1179812;  
 RA Sitihinggul P., Sarathongkum W., Longyant S., Panchan N.,  
 RA Sitihinggul W., Petsom A.;  
 RT "Three more novel FMRFamide-like neuropeptide sequences from the  
 eye stalk of the giant freshwater prawn Macrobryachium rosenbergii.",  
 RL Peptides 22:191-197(2001).  
 CC -1- MASS SPECTROMETRY: MW=1133.8; METHOD=MALDI.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 family.  
 CC GO: GO:0007218; P:neuropeptide signaling pathway; IDA.  
 DR KW Neuropeptide; Amidation.  
 FT MOD RES 9  
 SQ SEQUENCE 9 AA; 1133 MW; 845A0729C44441F5 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HN 10  
 Db 3 HN 4

## RESULT 14

UF02\_MOUSE

ID UF02\_MOUSE STANDARD; PRT; 9 AA.

AC P38610;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P32) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins  
 using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined PI of this unknown  
 protein is: 6.0, its MW is: 32 kDa.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1102 MW; 7E73EAB6D0581AAB CRC64;

Query Match 23.7%; Score 14; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EI Q 6  
 Db 4 EI Q 6

## RESULT 15

AL19\_CARMA

ID AL19\_CARMA STANDARD; PRT; 10 AA.

AC P81822;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 19.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorge A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 CC KW Neuropeptide; Amidation; Multigene family.  
 FT MOD RES 10  
 SQ SEQUENCE 10 AA; 1101 MW; 96687CDB5B69AB1 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;  
 Best Local Similarity 40.0%; Pred. No. 7.2e+03;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 HN LG 12  
 Db 5 MYSPG 9

Search completed: May 18, 2004, 10:02:33  
 Job time : 7.75 secs

Tue May 18 12:03:01 2004

us-09-730-174a-3.closed.rspt

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:55:20 ; Search time 30.25 Seconds  
(without alignments)  
125.164 Million cell updates/sec

Title: US-09-730-174A-3  
Perfect score: 59  
Sequence: 1 SVSEIQLMNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL.25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp Unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	45.8	11	13	Q9PS71	Q9PS71 agkistrodon
2	23	39.0	12	13	P82081	P82081 limodysast
3	20	33.9	8	13	P82082	P82082 limodysast
4	20	33.9	8	13	P82083	P82083 limodysast
5	20	33.9	12	13	P82085	P82085 limodysast
6	19	32.2	8	8	Q34909	Q34909 locusta mig
7	19	32.2	9	12	Q92766	Q92766 canine dist
8	19	32.2	9	12	Q71066	Q71066 canine dist
9	18	30.5	8	10	Q40659	Q40659 cryza sariv
10	18	30.5	10	12	Q9PXC3	Q9PXC3 hepatitis b
11	18	30.5	11	5	Q23876	Q23876 dicystostei
12	18	30.5	12	15	Q85631	Q85631 avian carc
13	17	28.8	7	6	Q28742	Q28742 oryctolagus
14	17	28.8	9	4	Q15891	Q15891 homo sapien
15	17	28.8	9	8	Q9GD12	Q9GD12 lipospadix
16	17	28.8	9	8	Q9GCV6	Q9GCV6 sclerosperm

17	17	28.8	11	8	Q35374	Q35374 paramecium
18	17	28.8	11	10	P82336	P82336 pisum sativ
19	17	28.8	11	13	Q9PS71	Q9PS71 fugu rubrip
20	16	27.1	7	13	Q8UJ20	Q8UJ20 gallus gall
21	16	27.1	8	3	Q05403	Q05403 saccharomyc
22	16	27.1	8	4	Q15894	Q15894 homo sapien
23	16	27.1	9	2	Q44377	Q44377 aeromonas t
24	16	27.1	9	2	Q44468	Q44468 aeromonas v
25	16	27.1	9	2	Q8RKU3	Q8RKU3 borrelia bu
26	16	27.1	9	2	Q43928	Q43928 aeromonas p
27	16	27.1	9	2	Q44001	Q44001 aeromonas e
28	16	27.1	9	2	Q9K4M6	Q9K4M6 staphylococ
29	16	27.1	9	10	Q9FXL0	Q9FXL0 lilium long
30	16	27.1	10	2	Q7WUJ1	Q7WUJ1 pseudomonas
31	16	27.1	10	13	P82080	P82080 limodysast
32	15	25.4	7	12	Q66205	Q66205 transmissib
33	15	25.4	8	13	P82079	P82079 limodysast
34	15	25.4	9	2	Q43860	Q43860 azotobacter
35	15	25.4	9	5	Q8WT19	Q8WT19 drosophila
36	15	25.4	10	6	Q9TS43	Q9TS43 sus scrofa
37	15	25.4	10	8	Q8WBR7	Q8WBR7 chaltophoru
38	15	25.4	10	11	Q61807	Q61807 mus musculu
39	15	25.4	11	6	Q9BDC8	Q9BDC8 pongo pygma
40	15	25.4	11	6	Q9BDQ9	Q9BDQ9 gorilla gor
41	15	25.4	11	6	Q9BDP0	Q9BDP0 pan troglod
42	15	25.4	11	6	Q9BDC9	Q9BDC9 pan paniscu
43	15	25.4	12	2	Q9X6Y0	Q9X6Y0 aquilex pyr
44	15	25.4	12	6	Q9TQY5	Q9TQY5 bos taurus
45	14	23.7	8	2	Q47273	Q47273 escherichia

## ALIGNMENTS

RESULT 1  
ID Q9PS71 PRELIMINARY; PRT; 11 AA.  
AC Q9PS71  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Fibrinolytic metalloproteinase (Fragment).  
OS Agkistrodon contortrix.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Agkistrodon.  
CX NCBI\_TaxID=8720;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=91378546; Pubmed=1898066;  
RX Guan A.L., Retzius A.D., Henderson G.N., Markland F.S.Jr.;  
RT "Purification and characterization of a fibrinolytic enzyme from venom  
RT of the southern copperhead snake (Agkistrodon contortrix  
RT contortrix)".  
RL Arch. Biochem. Biophys. 289:197-207(1991).  
FT NON TER 11  
FT 11  
SQ SEQUENCE 11 AA; 1209 MW; 7CA02D1D41E8772B CRC64;

Query Match 45.8%; Score 27; DB 13; Length 11;  
Best Local Similarity 71.4%; Pred. No. 1,4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QLMENLIG 12  
DB 4 ELGNLIG 10

RESULT 2  
ID P82081 PRELIMINARY; PRT; 12 AA.  
AC P82081  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBlrel. 13, last annotation update)  
 DE DYNASTIN 3.  
 OS Limodynastes terraereginae (Northern banjo frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 CC Limodynastes terraereginae.  
 NCBI\_TaxID=104894;  
 RN  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE-TITIAL GLAND;  
 RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 the banjo frogs Limodynastes terraereginae."  
 RT Limodynastes terraereginae."  
 RL Aust. J. Chem. 46:833-842(1993).  
 CC -1- MASS SPECTROMETRY: MM=1236; METHOD=FAB.  
 SQ SEQUENCE 12 AA; 1236 MW; 147AA70FDF472724 CRC64;

Query Match 39.9%; Score 23; DB 13; Length 12;  
 Best Local Similarity 66.7%; Pred. NO. 1e+03;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 LMNLG 12  
 DB 6 LKMLG 11

RESULT 3  
 ID P82082 PRELIMINARY; PRT; 8 AA.  
 AC P82082;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)  
 DE DYNASTIN 4.  
 OS Limodynastes salmuni (Salmun's-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 CC Limodynastes salmuni.  
 NCBI\_TaxID=39404;  
 RN  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 Limodynastes salmuni and Fletcherin from Limodynastes Fletcheri."  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -1- MASS SPECTROMETRY: MM=772; METHOD=FAB.  
 SQ SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;

Query Match 33.9%; Score 20; DB 13; Length 8;  
 Best Local Similarity 66.7%; Pred. NO. 1e+06; 1;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMNLG 12  
 DB 2 LKMLG 7

RESULT 4  
 ID P82083 PRELIMINARY; PRT; 8 AA.  
 AC P82083;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)  
 DE DYNASTIN 5.  
 OS Limodynastes salmuni (Salmun's-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 CC Limodynastes salmuni.  
 NCBI\_TaxID=39404;  
 RN  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE-TITIAL GLAND;  
 RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 the banjo frogs Limodynastes terraereginae."  
 RT Limodynastes terraereginae."  
 RL Aust. J. Chem. 46:833-842(1993).  
 CC -1- MASS SPECTROMETRY: MM=1236; METHOD=FAB.  
 SQ SEQUENCE 12 AA; 1236 MW; 147AA70FDF472724 CRC64;

RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 Limodynastes salmuni and Fletcherin from Limodynastes Fletcheri."  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -1- MASS SPECTROMETRY: MM=786; METHOD=FAB.  
 SQ SEQUENCE 8 AA; 786 MW; 7B58772455B05728 CRC64;

Query Match 33.9%; Score 20; DB 13; Length 8;  
 Best Local Similarity 66.7%; Pred. NO. 1e+06; 1;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMNLG 12  
 DB 2 LKMLG 7

RESULT 5  
 ID P82085 PRELIMINARY; PRT; 12 AA.  
 AC P82085;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)  
 DE DYNASTIN 7.  
 OS Limodynastes salmuni (Salmun's-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 CC Limodynastes salmuni.  
 NCBI\_TaxID=39404;  
 RN  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 Limodynastes salmuni and Fletcherin from Limodynastes Fletcheri."  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -1- MASS SPECTROMETRY: MM=1114; METHOD=FAB.  
 SQ SEQUENCE 12 AA; 1114 MW; 3AB5A976CAA72728 CRC64;

Query Match 33.9%; Score 20; DB 13; Length 12;  
 Best Local Similarity 66.7%; Pred. NO. 4.3e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMNLG 12  
 DB 6 LKMLG 11

RESULT 6  
 ID Q34909 PRELIMINARY; PRT; 8 AA.  
 AC Q34909;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)  
 DE Cytochrome b (Fragment).  
 OS Locusta migratoria (Migratory locust).  
 CC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
 CC Acrididae; Oedipodinae; Locusta.  
 NCBI\_TaxID=7004;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88223478; PubMed=2836084;  
 RA McCracken A., Unkenbusch I., Gellissen G.;  
 RT "Structure of the cloned locusta migratoria mitochondrial genome:  
 restriction mapping and sequence of its ND-1 (URF-1) gene."  
 RL Curr. Genet. 11:625-630(1987).  
 CC EMBL; X05286; CAA28905.1;  
 DR GO; GO:0005739; C:mitochondrion; IEA.

KM Mitochondrion.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 32.2%; Score 19; DB 8; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSEIQLMH 9  
 DB 1 MSYIKLKH 8

RESULT 7  
 ID 092766 PRELIMINARY; PRT; 9 AA.

AC 092766;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE Fusion protein (Fragment).

OS Canine distemper virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses;  
 OX NCBI\_TaxID=11232;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dog #5526/89;  
 RA Lieberman H., Harder T., Haas L.;  
 RT "Genetic analysis of the central untranslated genome region and the proximal coding part of the F gene of wild-type and vaccine distemper morbilliviruses";  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026237; AAC09167.1; -;  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;

Query Match 32.2%; Score 19; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MEN 10  
 DB 1 MEN 3

RESULT 8  
 ID 071066 PRELIMINARY; PRT; 9 AA.

AC 071066;  
 DT 01-AUG-1998 (TREMBlrel. 07, Created)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Fusion protein (Fragment).

OS Canine distemper virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses;  
 OX NCBI\_TaxID=11232;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dog #10757/96;  
 RA Lieberman H., Harder T., Haas L.;  
 RT "Genetic analysis of the central untranslated genome region and the proximal coding part of the F gene of wild-type and vaccine distemper morbilliviruses";  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026234; AAC09164.1; -;  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;

Query Match 32.2%; Score 19; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MEN 10  
 DB 1 MEN 3

RESULT 9  
 ID 040659 PRELIMINARY; PRT; 8 AA.

AC 040659;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Alpha-amylase (Rice).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzoae; Oryza.  
 OX NCBI\_TaxID=4530;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=1078641; PubMed=2258052;  
 RA Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R., Rodriguez R.L.;  
 RT "Expression and secretion of rice alpha-amylase by saccharomyces cerevisiae";  
 RL Gene 94:209-216(1990).  
 DR EMBL; M62916; AAA33892.1; -;  
 DR Gramene; Q40659; -;  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;

Query Match 30.5%; Score 18; DB 10; Length 8;  
 Best Local Similarity 28.6%; Pred. No. 1e+06;  
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 5 IOLMH 11  
 DB 1 MOVUNNM 7

RESULT 10  
 ID 09PX3 PRELIMINARY; PRT; 10 AA.

AC 09PX3;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE E antigen P20E (Fragment).

OS Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;

RN [1]  
 RP SEQUENCE  
 RX MEDLINE=92013147; PubMed=1717588;  
 RA Takahashi K., Kishimoto S., Ohoi K., Yoshizawa H., Machida A., Ohnuma H., Tsuda F., Muneakata E., Miyakawa Y., Mayumi M.;  
 RT "Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepatitis B virus";  
 RL J. Immunol. 147:3156-3160(1991).

DR PIR; B46453; B46453.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1238 MW; 485A6E3AE721E9C7 CRC64;

Query Match 30.5%; Score 18; DB 12; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 IOLMH 9



Db 1 MOLF 5

## RESULT 11

Q23976 ID Q23976 PRELIMINARY; PRT; 11 AA.  
 AC Q23976;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)  
 DE Actin 4.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82260445; PubMed=6286214;  
 RA McKeeown M., Firtel R.A.;  
 RT "Actin multigene family of Dictyostelium";  
 RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).  
 DR EMBL; K02957; AAA3150.1; -.  
 DR EMBL; K02956; AAA3150.1; JOINED.  
 SQ SEQUENCE 11 AA; 1205 MW; 728B4C14C6C2CAAB CRC64;

Query Match 30.5%; Score 18; DB 5; Length 11;  
 Best Local Similarity 28.6%; Pred. No. 1e+04;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 EIQMLNN 10  
 Db 5 DVQALNN 11

## RESULT 12

Q85631 ID Q85631 PRELIMINARY; PRT; 12 AA.  
 AC Q85631;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
 DE MH2, proviral DNA, myc to 3' UTR (Fragment).  
 OS Avian carcinoma virus.  
 OX Viruses; Retroviridae; Retroviridae; Alpharetrovirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85033920; PubMed=6092695;  
 RA Strive P., Jansen H.W., Bister K., Rapp U.R.;  
 RT "3'-terminal region of avian carcinoma virus MH2 shares sequence elements with avian sarcoma viruses Y73 and SR-A.";  
 RL J. Virol. 52:703-705(1984).  
 DR EMBL; K03100; AAA2388.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1466 MW; 72E4B884F30736DB CRC64;

Query Match 30.5%; Score 18; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNL 11  
 Db 2 HNL 4

RESULT 13  
 Q28742 ID Q28742 PRELIMINARY; PRT; 7 AA.  
 AC Q28742;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)  
 DE Alpha-myosin heavy chain (Fragment).  
 OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=84221901; PubMed=6328491;  
 RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,  
 RA Rabinowitz M.;  
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-  
 ventricular myosin heavy chains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).  
 DR EMBL; K01698; AAA31415.1; -.  
 DR PIR; I46868; I46868.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 916 MW; 6B1B1A1E69326B0 CRC64;

Query Match 28.8%; Score 17; DB 6; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QLMNN 10  
 Db 1 QXQHD 5

## RESULT 14

Q15891 ID Q15891 PRELIMINARY; PRT; 9 AA.  
 AC Q15891;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
 DE (Clone XP2B8B) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta.  
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.I., Chinnail C.A., Baldwin A., Lindsay E.A., Zhao Z.-Y.,  
 RA Gaeky C.T.H.;  
 RT "Isolation of chromosome-specific genes by reciprocal probing of  
 RT arrayed cDNAs and cosmid libraries.";  
 RL Hum. Mol. Genet. 0:0-0(1995).  
 DR EMBL; L32131; AAA73881.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 9 AA; 1030 MW; E56635A1A3366D1 CRC64;

Query Match 28.8%; Score 17; DB 4; Length 9;  
 Best Local Similarity 44.4%; Pred. No. 1e+06;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 EIQMLNLG 12  
 Db 1 EHQMKSTLG 9

## RESULT 15

Q96D12 ID Q96D12 PRELIMINARY; PRT; 9 AA.  
 AC Q96D12;  
 DT 01-MAR-2001 (TEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)  
 DE Ribosomal protein S16 (Fragment).  
 GN RPS16.  
 OS Linozpadix monostachya.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecaceae;

OC Areceae; Línospadiciinae; Línospadix.  
OX NCBI\_TaxID=131282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RA Asmussen C.B., Chase M.W.;  
RT "Coding and noncoding plastid DNA in palm systematics.";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ404941; CAC17917.1; -  
DR GO; GO:0009507; Chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1106 MW; 1B9236C2C0441B50 CRC64;  
Query Match 28.8%; Score 17; DB 8; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1e+06;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 IQLM 8  
Db 6 VQLM 9

Search completed: May 18, 2004, 10:04:47  
Job time : 32.25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:42:39 ; Search time 45.75 Seconds  
(without alignments)  
74.111 Million cell updates/sec

Title: US-09-730-174A-3  
Perfect score: 59  
Sequence: 1 SEVEIQLMNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	84.7	11	3	AA96968 Parathyro
2	50	84.7	11	6	ABG72607 Parathyro
3	50	84.7	12	6	ABG72608 Parathyro
4	49	83.1	10	2	AA91644 Human par
5	49	83.1	10	3	AA91647 Human aci
6	49	83.1	10	4	AA86219 Human par
7	49	83.1	10	6	ABR44166 Human par
8	45	76.3	9	4	AA86225 Human par
9	43	72.9	9	2	AA91645 Human par
10	43	72.9	9	3	AA96981 Parathyro
11	43	72.9	9	4	AA86220 Human par
12	40.5	68.6	11	2	AA95060 Resin bou
13	40	67.8	9	3	AA801862 PTH(1-14)
14	40	67.8	9	3	AA96966 Parathyro
15	37	62.7	9	3	AA801863 PTH(1-14)
16	37	62.7	10	4	AA96932 Rat parat
17	37	62.7	11	4	AA96931 Rat parat
18	37	62.7	11	4	AA96935 Parathyro
19	37	62.7	11	4	AA84770 Parathyro
20	37	62.7	12	4	AA96914 Parathyro
21	37	62.7	12	4	AA84769 Parathyro
22	36	61.0	9	3	AA978849 Parathyro
23	35	59.3	8	2	AA91646 Human par
24	35	59.3	8	3	AA91646 Human par
25	35	59.3	8	4	AA86221 Human par

26	35	59.3	10	6	ABP71484 Parathyro
27	35	59.3	11	6	ABP71485 Parathyro
28	35	59.3	11	6	ABP71483 Parathyro
29	35	59.3	12	6	AAW45785 Parathyro
30	35	59.3	12	6	ABP71482 Parathyro
31	33	55.9	9	3	AA801866 PTH(1-14)
32	32	54.2	11	1	AA982547 (Asn10, T
33	32	54.2	11	4	AA96982 Rat parat
34	32	54.2	12	4	AA96981 Rat parat
35	30	50.8	7	2	AA91647 Human par
36	30	50.8	7	4	AA86222 Human par
37	30	50.8	9	3	AA801864 PTH(1-14)
38	30	50.8	9	3	AA97062 PTH-rp N-
39	29	49.2	10	5	ABG69386 Vascular
40	29	49.2	12	5	AAU93357 Granulocy
41	27	45.8	11	4	ABU54029 Human DNA
42	27	45.8	12	2	AA889301 Japanese
43	27	45.8	12	3	AA821270 Fertilin
44	26	44.1	6	2	AA91648 Human par
45	26	44.1	6	3	AA968764 Amino aci

## ALIGNMENTS

RESULT 1  
AA96968 standard; peptide; 11 AA.

AA96968 standard; peptide; 11 AA.  
AC AA96968;  
DT 31-OCT-2000 (first entry)  
DE Parathyroid hormone N-terminal signaling domain (residues 1-11).  
XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
KM bone reformation; resorption; remodeling; tether1; osteoporosis.  
XX Homo sapiens.  
XX WO200039278-A2.  
XX 06-JUL-2000.  
XX 30-DEC-1999; 99WO-US031108.  
XX 31-DEC-1998; 98US-0114577P.  
XX (GARD/) GARDELLA T J.  
XX (KRON/) KRONENBERG H M.  
XX (BOT/) BOTTS J T.  
XX (JUEP/) JUEPPNER H.  
XX Gardella TV, Kronenberg HM, Fotts JT, Jueppner H;  
XX WPI; 2000-452384/39.  
XX New compound comprising an amino terminal signaling functional domain  
XX linked to a carboxy-terminal binding portion of parathyroid hormone for  
XX treating mammalian conditions characterized by decreases in bone mass.  
XX Claim 4; Page 92; 119pp; English.  
XX Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or S-(L) n  
XX -R, are new S is an amino terminal signaling functional domain of  
XX parathyroid hormone (PTH); L is a linker molecule present n times (where  
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the  
XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
XX sequence. The new compounds are used for treating mammalian conditions  
XX characterized by decreases in bone mass, determining rates of bone  
XX reformation, bone resorption and/or bone remodeling, treating diseases  
XX and disorders associated with decreased rethet1 activity, increasing cAMP



XX The invention relates to a new antigenic peptide for inducing the  
CC formation and isolation of antibodies having an affinity to it, being  
CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
CC are: (1) a method for producing antibodies useful in the determination of  
CC PTH levels in a biological sample comprising: (a) providing at least one  
CC first peptide antigen comprising a peptide fragment of PTH; (b)  
CC administering the first peptide antigen to a host animal to induce  
CC antibody production; (c) monitoring the antibody titre produced; (d)  
CC isolating antisera produced in the host animal; and (e) selecting  
CC antisera from the isolated antisera produced in the host that is capable  
CC of binding to a second peptide antigen; (2) an antibody (ab) produced by  
CC the method; and (3) test kits and analytical procedures used for the  
CC determination of bioactive intact PTH utilising (ab). The methods and  
CC compositions of the present invention are useful for determining  
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
CC The antigens, antibodies and methods of the present invention, as  
CC compared to prior art, have the particular advantages of possessing  
CC greater affinity for PTH, and in particular, are designed to have a novel  
CC recognition for amino acid residues extending beyond the first N-terminal  
CC PTH residue, and further have negligible cross-reactivity with the large  
CC non-molecular forms of PTH. PTH levels are an important parameter in  
CC patients suffering from hypercalcaemia, osteoporosis and primary  
CC hyperparathyroidism. The present sequence represents a PTH antigenic  
CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,  
CC canine and bovine PTH  
CC  
CC  
SQ Sequence 12 AA;  
Query Match 84.7%; Score 50; DB 6; Length 12;  
Best Local Similarity 90.9%; Pred. No. 0.014; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 VSEIQMLNMG 12  
DB 2 VSEIQMLNMG 12  
RESULT 4  
AAR91644  
ID AAR91644 standard; peptide; 10 AA.  
AC AAR91644;  
XX  
XX 06-NOV-1996 (first entry)  
DT  
XX Human parathyroid hormone antigenic peptide hPTH 1-10.  
DE  
XX Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
KW  
XX diagnosis; active hPTH 1-37.  
OS  
XX Synthetic.  
XX  
XX DE4434551-A1.  
XX PD 04-APR-1996.  
XX PF 26-SEP-1994; 94DE-04434551.  
XX PR 28-SEP-1994; 94DE-04434551.  
XX PA (FORS/) FORSSMANN W.  
XX  
XX Adermann K, Forssmann W, Hock D, Maegerlein M;  
XX WPI; 1996-180391/19.  
XX  
XX New antigenic peptide(s) from human parathyroid hormone - and antibodies  
XX generated using them, able to distinguish between active and inactive  
XX forms of the hormone.  
XX  
XX Claim 2; Page 4; 5pp; German.  
XX

CC The present sequence is a specific example of claimed immunogenic  
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-  
CC terminal alpha-helical region and/or the non-structured region of the  
CC hormone. Antibodies and their binding fragments generated by injecting an  
CC animal with the peptides are useful as diagnostic reagents for  
CC determination of biologically active hPTH(1-37)  
CC  
CC  
SQ Sequence 10 AA;  
Query Match 83.1%; Score 49; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVSEIQMLNHN 10  
DB 1 SVSEIQMLNHN 10  
RESULT 5  
AAV68767  
ID AAV68767 standard; peptide; 10 AA.  
XX  
AC AAV68767;  
XX  
DT 05-MAY-2000 (first entry)  
DE  
XX Amino acids 1-10 of a parathyroid hormone (PTH).  
DE  
XX Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;  
KW  
XX slimming treatment; cellulite; skin firming.  
XX  
OS Unidentified.  
XX  
XX WO200004047-A1.  
XX PD 27-JAN-2000.  
XX PF 07-JUL-1999; 99WO-FR001687.  
XX PR 17-JUL-1998; 98FR-00009193.  
XX  
XX (SEDE-) SEDERMA.  
XX  
XX Lintner K;  
XX  
XX WPI; 2000-171243/15.  
DR  
XX New parathyroid hormone fragment peptides, used as lipolysis stimulants  
PT in topically applied cosmetic compositions for slimming treatment of  
PT excessive weight in hips and thighs.  
XX  
XX Claim 1; Page 6; 18pp; French.  
XX  
XX The present sequence represents a parathyroid hormone (PTH) fragment,  
CC comprising amino acids 1-10. Parathyroid hormone fragments of the  
CC invention have lipolytic stimulating activity (especially when topically  
CC administered). The lipolytic activity of the peptides is enhanced when  
CC they are chemically modified to increase their lipophilicity. The  
CC peptides are used in cosmetic or dermatological compositions for skin  
CC care. They are especially used for slimming treatment of excessive weight  
CC in the thighs and hips, in the treatment of cellulite and for skin  
CC firming  
CC  
CC  
SQ Sequence 10 AA;  
Query Match 83.1%; Score 49; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVSEIQMLNHN 10  
DB 1 SVSEIQMLNHN 10

RESULT 6  
 AAB86219  
 ID AAB86219 standard; peptide; 10 AA.  
 AC AAB86219;  
 DT 03-SEP-2001 (first entry)  
 DE Human parathyroid hormone immunogenic peptide SEQ ID 1.  
 KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
 KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
 KW hypo-parathyroidism; hyper-parathyroidism.  
 OS Homo sapiens.  
 XX DE1961350-A1.  
 XX 21-JUN-2001.  
 XX 17-DEC-1999; 99DE-01061350.  
 XX 17-DEC-1999; 99DE-01061350.  
 XX 17-DEC-1999; 99DE-01061350.  
 XX (IMMU-) IMMUNODIAGNOSTIK AG.  
 XX Amburster FP;  
 XX WPI; 2001-376318/40.  
 XX Determining the content of physiologically active parathyroid hormone,  
 PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
 PT reactive with different epitopes.  
 XX  
 XX Disclosure; Page 3; 10pp; German.  
 XX  
 CC This invention describes a novel method for determining (M1) the content  
 CC of active parathyroid hormone (A) by treating a sample with (i) antibody  
 CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
 CC and including the N-terminal residue and (ii) antibody (Ab2) that  
 CC recognizes an epitope within the receptor-binding site of (A). The number  
 CC of molecules that react with both antibodies is determined and used to  
 CC calculate the content of physiologically active (A). The method is used  
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
 CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
 CC active and (ii) that apparently intact peptide may be biologically  
 CC inactive, and also takes into account the fact that some fragments of (A)  
 CC are antagonistic (these have the receptor-binding site but lack the N-  
 CC terminus). It thus provides a true measure of the content of  
 CC physiologically active (A), contrast methods that measure intact peptide  
 CC and its 1-37 fragment which may produce falsely high values. This  
 CC sequence represents a peptide fragment used to illustrate the method of  
 CC the invention  
 XX  
 XX Sequence 10 AA;  
 SQ

Query March 83.1%; Score 49; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Gaps 0;  
 Matches 10; Conservative 0; Indels 0; Gaps 0;  
 QY 1 SVSEIQLMHN 10  
 DB 1 SVSEIQLMHN 10  
 RESULT 7  
 ABR44166  
 ID ABR44166 standard; peptide; 10 AA.  
 XX  
 XX ABR44166;  
 XX

DT 04-AUG-2003 (first entry)  
 DE Human parathyroid hormone (hPTH) fragment (residues 1-10).  
 XX  
 XX Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;  
 KW lipolysis; human; hPTH.  
 XX  
 OS Homo sapiens.  
 XX WO2003035697-A1.  
 XX 01-MAY-2003.  
 XX 06-MAY-2002; 2002WO-KR000835.  
 XX 27-SEP-2001; 2001KR-00060245.  
 XX 15-MAR-2002; 2002KR-00014062.  
 XX (GLDS ) LG HOUSEHOLD & HEALTH CARE LTD.  
 XX Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H,  
 XX Chang M;  
 XX WPI; 2003-468288/44.  
 XX Novel fusion peptide comprising self cell-penetrating Tat peptide bound  
 PT to human parathyroid hormone-derived peptide, useful as component of skin  
 PT slimming cosmetic composition.  
 XX  
 XX Claim 5; Page 6; 32pp; English.  
 XX  
 CC The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-  
 CC penetrating Tat peptide is bound to human parathyroid hormone-derived  
 CC peptide (hPTHDP). The fusion peptide is useful as a component of skin  
 CC slimming cosmetic composition. The fusion peptide does not cause  
 CC irritation, easily and safely penetrates into integument and endothelium,  
 CC does not cause skin disease and has superior lipolysis effects, and is  
 CC durable. The present sequence represents a human parathyroid hormone  
 CC (hPTH) fragment that can be used to construct the fusion peptide  
 CC  
 XX Sequence 10 AA;  
 SQ

Query March 83.1%; Score 49; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Gaps 0;  
 Matches 10; Conservative 0; Indels 0; Gaps 0;  
 QY 1 SVSEIQLMHN 10  
 DB 1 SVSEIQLMHN 10

RESULT 8  
 AAB86225  
 ID AAB86225 standard; peptide; 9 AA.  
 AC AAB86225;  
 DT 03-SEP-2001 (first entry)  
 DE Human parathyroid hormone immunogenic peptide SEQ ID 7.  
 KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
 KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
 KW hypo-parathyroidism; hyper-parathyroidism.  
 OS Homo sapiens.  
 XX DE1961350-A1.  
 XX 21-JUN-2001.  
 XX 17-DEC-1999; 99DE-01061350.  
 XX

PR 17-DEC-1999; 99DE-01061350.  
XX (IMMU-) IMMUNDIAGNOSTIK AG.  
XX  
XX  
PI Ambuster FP;  
DR WPI; 2001-376318/40.  
XX  
XX  
PT Determining the content of physiologically active parathyroid hormone,  
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
PT reactive with different epitopes.  
XX  
XX  
PS Disclosure; Page 3; 10pp; German.  
XX  
XX  
CC This invention describes a novel method for determining (M1) the content  
CC of active parathyroid hormone (A) by treating a sample with (i) antibody  
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
CC and including the N-terminal residue and (ii) antibody (Ab2) that  
CC recognizes an epitope within the receptor-binding site of (A). The number  
CC of molecules that react with both antibodies is determined and used to  
CC calculate the content of physiologically active (A). The method is used  
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
CC active and (ii) that apparently intact peptide may be biologically  
CC inactive, and also takes into account the fact that some fragments of (A)  
CC are antagonistic (these have the receptor-binding site but lack the N-  
CC terminus). It thus provides a true measure of the content of  
CC physiologically active (A); contrast methods that measure intact peptide  
CC and its 1-37 fragment which may produce falsely high values. This  
CC sequence represents a peptide fragment used to illustrate the method of  
CC the invention  
XX  
SQ Sequence 9 AA;  
XX  
XX  
Query Match 76.3%; Score 45; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VSEIQLMNH 10  
DB 1 VSEIQLMNH 9  
XX  
XX  
RESULT 9  
AAR91645  
ID AAR91645 standard; peptide; 9 AA.  
XX  
XX  
AC AAR91645;  
XX  
XX  
DT 06-NOV-1996 (first entry)  
XX  
XX  
DE Human parathyroid hormone antigenic peptide hPTH 1-9.  
XX  
XX  
KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
KW diagnosis; active hPTH 1-37.  
XX  
XX  
OS Synthetic.  
XX  
XX  
PN DE434551-A1.  
XX  
XX  
PD 04-APR-1996.  
XX  
XX  
PF 28-SEP-1994; 94DE-04434551.  
XX  
XX  
PR 28-SEP-1994; 94DE-04434551.  
XX  
XX  
PA (FORS/) FORSSMANN W.  
XX  
XX  
PI Adertmann K, Forssmann W, Hock D, Maegerlein M;  
XX  
XX  
DR WPI; 1996-180391/19.

PT New antigenic peptide(s) from human parathyroid hormone - and antibodies  
PT generated using them, able to distinguish between active and inactive  
PT forms of the hormone.  
XX  
XX  
PS Claim 2; Page 4; 5pp; German.  
XX  
XX  
CC The present sequence is a specific example of claimed immunogenic  
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-  
CC terminal alpha-helical region and/or the non-structured region of the  
CC hormone. Antibodies and their binding fragments generated by injecting an  
CC animal with the peptides are useful as diagnostic reagents for  
CC determination of biologically active hPTH(1-37)  
XX  
XX  
SQ Sequence 9 AA;  
XX  
XX  
Query Match 72.9%; Score 43; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VSEIQLMNH 9  
DB 1 VSEIQLMNH 9  
XX  
XX  
RESULT 10  
AA96981  
ID AA96981 standard; peptide; 9 AA.  
XX  
XX  
AC AA96981;  
XX  
XX  
DT 31-OCT-2000 (first entry)  
XX  
XX  
DE Parathyroid hormone N-terminal signaling domain.  
XX  
XX  
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
KW bone reformation; resorption; remodeling; tether1; osteoporosis.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
FN WO200039278-A2.  
XX  
XX  
PD 06-JUL-2000.  
XX  
XX  
PF 30-DEC-1999; 99MO-US031108.  
XX  
XX  
PR 31-DEC-1998; 98US-0114577P.  
XX  
XX  
PA (GARD/) GARDELLA T J.  
PA (KRON/) KRONENBERG H M.  
PA (POT/) POTTS J T.  
PA (JUEP/) JUEPPNER H.  
XX  
XX  
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX  
XX  
DR WPI; 2000-452384/39.  
XX  
XX  
PT New compound comprising an amino terminal signaling functional domain  
PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
PT treating mammalian conditions characterized by decreases in bone mass.  
XX  
XX  
PS Claim 11; Page 93; 119pp; English.  
XX  
XX  
CC Compounds of the structure or formula S-(L)-n-B, R1-S-(L)-n-R or S-(L)-n  
CC -R, are new. S is an amino terminal signaling functional domain of  
CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the  
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
CC sequence. The new compounds are used for treating mammalian conditions  
CC characterized by decreases in bone mass, determining rates of bone  
CC reformation, bone resorption and/or bone remodeling, treating diseases  
CC and disorders associated with decreased tether1 activity, increasing cAMP  
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or

CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
 CC regular injections to treat osteoporosis

XX Sequence 9 AA;

Query Match 72.9%; Score 43; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9  
 DB 1 SVSEIQLMH 9

RESULT 11  
 ID AAB86220 standard; peptide: 9 AA.

XX AAB86220;  
 AC AAB86220;  
 XX 03-SEP-2001 (first entry)

XX Human parathyroid hormone immunogenic peptide SEQ ID 2.

XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
 KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
 KM hypo-parathyroidism; hyper-parathyroidism.

XX Homo sapiens.

XX DE19961350-A1.

XX 21-JUN-2001.

XX 17-DEC-1999; 99DE-01061350.

XX 17-DEC-1999; 99DE-01061350.

XX (IMMU-) IMMUNDIAGNOSTIK AG.

XX Armbruster FP;

XX WPI; 2001-376318/40.

XX Determining the content of physiologically active parathyroid hormone,  
 PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
 FT reactive with different epitopes.

XX Disclosure; Page 3; 10pp; German.

XX This invention describes a novel method for determining (M) the content  
 CC of active parathyroid hormone (A) by treating a sample with (i) antibody  
 CC (Aa1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
 CC and including the N-terminal residue and (ii) antibody (Ab2) that  
 CC recognizes an epitope within the receptor-binding site of (A). The number  
 CC of molecules that react with both antibodies is determined and used to  
 CC calculate the content of physiologically active (A). The method is used  
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
 CC (i) some fragments of (A) shorter than the complete (64 aa) peptide are  
 CC active and (ii) that apparently intact peptide may be biologically  
 CC inactive, and also takes into account the fact that some fragments of (A)  
 CC are antagonistic (these have the receptor-binding site but lack the N-  
 CC terminus). It thus provides a true measure of the content of  
 CC physiologically active (A); contrast methods that measure intact peptide  
 CC and its 1-37 fragment which may produce falsely high values. This  
 CC sequence represents a peptide fragment used to illustrate the method of  
 CC the invention

XX Sequence 9 AA;

Query Match 72.9%; Score 43; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9  
 DB 1 SVSEIQLMH 9

RESULT 12  
 ID AAY50600 standard; peptide: 11 AA.

XX AAY50600;  
 AC AAY50600;  
 XX 09-FEB-2000 (first entry)

XX Resin bound cyclic peptide 33.

XX Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;  
 KW hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;  
 KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;  
 KM Cushing's syndrome; renal failure; hypertension; bone fracture repair.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "FMOC-Ala"

FT Misc-difference 3 /note= "Ser(OrBu)"

FT Misc-difference 4 /note= "Glu(OrBu)"

FT Misc-difference 6 /note= "Gln(Trt)"

FT Misc-difference 9 /note= "His(Trt)"

FT Misc-difference 10 /note= "Asn(Trt)"

XX WO9552933-A1.

XX 21-OCT-1999.

XX 15-APR-1999; 99WO-US008435.

XX 15-APR-1998; 98US-0081897P.

XX (RHON ) RHONE-POULENC RORER PHARM INC.

XX Sledeski AW, Mancel JU;

XX WPI; 1999-633822/54.

XX Convergent synthesis of peptides for treating e.g. bone disorders.

XX Disclosure; Page 75; 85pp; English.

XX This invention describes a novel method for the preparation of peptides  
 CC (ii) that contain both cyclic and linear peptide fragments comprises  
 CC sequential reaction of a resin-bound linear fragment with the cyclic  
 CC fragment in N-protected form and optionally other linear fragments. The  
 CC products of the invention have osteopathic and hypotensive activity (ii)  
 CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The  
 CC method is particularly used to prepare cyclic peptide analogs of  
 CC parathyroid hormone (PTH) or PTH-related peptides which are useful for  
 CC treating diseases that respond to treatment with agents that bind to PTH  
 CC receptors (with or without activation of adenyl cyclase activity), e.g.  
 CC hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-  
 CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also  
 CC for promoting repair of bone fractures. Separate syntheses of the cyclic  
 CC fragment allows convergent synthesis of resin-bound (ii), with better  
 CC yields and higher throughput. The difficulties associated with  
 CC preparation of the bridged fragment are confined to a small peptide which



CC can be purified before reaction with the resin-bound component. AAY50568-  
CC Y50614 represent the peptide fragments described in the method of the  
CC invention.  
XX  
SQ Sequence 11 AA;  
Query Match 68.6%; Score 40.5; DB 2; Length 11;  
Best Local Similarity 83.3%; Pred. No. 0.73;  
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
QY 1 SVSEIQLMH 12  
:|||||  
DB 1 AVSEIQLMH 11  
RESULT 13  
AAB01862  
ID AAB01862 standard; peptide; 9 AA.  
XX  
AC AAB01862;  
XX  
DT 11-SEP-2000 (first entry)  
XX PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.  
XX  
DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.  
XX  
KW Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;  
KW calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;  
KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200023594-A1.  
XX  
PD 27-APR-2000.  
XX  
PF 20-OCT-1999; 99WO-US024461.  
XX  
PR 22-OCT-1998; 98US-0105530P.  
XX  
PA (GARD/) GARDELLA T J.  
PA (KRON/) KRONENBERG H M.  
PA (POT/) POTTS J T.  
PA (JUEP/) JUEPPNER H.  
PI Gardeila TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX  
XX WPI; 2000-339693/29.  
XX  
XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
PT acids that encode them, useful for treating osteoporosis.  
XX  
XX Disclosure; Page 26; 73pp; English.  
XX  
XX The invention relates to a novel parathyroid hormone (PTH) peptide  
CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and  
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
CC B01869). The peptides of the invention are at least 65% identical to the  
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-  
CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
CC provided that the peptide is not PTHrP(1-14). The peptides of the  
CC invention also encompass fragments of peptides of the invention  
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,  
CC and is necessary for the normal function of the gastrointestinal,  
CC skeletal, neurological system, neuromuscular and cardiovascular systems.  
CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
CC effect on the skeleton, and mediates calcium reabsorption, enhances  
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous  
CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
CC the renal and skeletal actions of PTH, and also bind to the PTH-1

CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01859,  
CC AAB01861-B01869) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
CC conditions characterized by a decrease in bone mass, such as  
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
CC medical disorders that arise from excessive or altered action of the PTH-  
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
CC useful in the determination of rates of bone formation, bone resorption  
CC and/or bone remodelling in a patient. The peptides of the invention are  
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
CC conventional synthetic chemistry, and can be delivered to a patient via  
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
CC PTH-1/PTH-2 receptor agonists  
XX  
SQ Sequence 9 AA;  
Query Match 67.8%; Score 40; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVSEIQLMH 9  
:|||||  
DB 1 AVSEIQLMH 9  
RESULT 14  
AAY6966  
ID AAY6966 standard; peptide; 9 AA.  
XX  
AC AAY6966;  
XX  
DT 31-OCT-2000 (first entry)  
XX  
DE Parathyroid hormone N-terminal signaling domain (residues 1-9).  
XX  
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
KW bone reformation; resorption; remodeling; tether1; osteoporosis.  
XX  
OS Homo sapiens.  
OS  
XX  
PN WO200039278-A2.  
XX  
PD 06-JUL-2000.  
XX  
PF 30-DEC-1999; 99WO-US031108.  
XX  
PR 31-DEC-1998; 98US-0114577P.  
XX  
PA (GARD/) GARDELLA T J.  
PA (KRON/) KRONENBERG H M.  
PA (POT/) POTTS J T.  
PA (JUEP/) JUEPPNER H.  
PI Gardeila TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX  
XX WPI; 2000-452364/39.  
XX  
XX New compound comprising an amino terminal signaling functional domain  
PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
PT treating mammalian conditions characterized by decreases in bone mass.  
XX  
PS Claim 4; Page 92; 119pp; English.  
XX  
XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n  
CC -R are new. S is an amino terminal signaling functional domain of  
CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the  
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
CC sequence. The new compounds are used for treating mammalian conditions  
CC characterized by decreases in bone mass, determining rates of bone  
CC reformation, bone resorption and/or bone remodeling, treating diseases

CC and disorders associated with decreased tether1 activity, increasing cAMP  
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
CC regular injections to treat osteoporosis  
XX

Sequence 9 AA:

Query Match 67.8%; Score 40; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9  
Db 1 AVSEIQLMH 9

RESULT 15

AAB01863 standard; peptide; 9 AA.

AC AAB01863;

DT 11-SEP-2000 (first entry)

PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.

Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;

calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;

bone synthesis; agonist; osteoporosis; non-parenteral delivery.

Homo sapiens.

Synthetic.

27-APR-2000.

20-OCT-1999; 99WO-US024481.

22-OCT-1998; 98US-0105530P.

(GARD/) GARDILA T J.

(KRON/) KRONENBERG H M.

(POT/) POTTS J T.

(JUEP/) JUEPNER H.

Gardella TJ, Kronenberg HM, Potts JT, Juepner H;

WPI: 2000-339693/29.

Disclosure; Page 26; 73pp; English.

XX The invention relates to a novel parathyroid hormone (PTH) peptide  
CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and  
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
CC B01869). The peptides of the invention are at least 85% identical to the  
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-  
CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
CC provided that the peptide is not PTHrP(1-14). The peptides of the  
CC invention also encompass fragments of peptides of the invention  
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,  
CC and is necessary for the normal function of the gastrointestinal,  
CC skeletal, neurological system, neuromuscular and cardiovascular systems.  
CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
CC effect on the skeleton, and mediates calcium reabsorption, enhances  
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous

CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
CC the renal and skeletal actions of PTH, and also bind to the PTH-1  
CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
CC conditions characterized by a decrease in bone mass, such as  
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
CC medical disorders that arise from excessive or altered action of the PTH-  
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
CC useful in the determination of rates of bone formation, bone resorption  
CC and/or bone remodeling in a patient. The peptides of the invention are  
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
CC conventional synthetic chemistry, and can be delivered to a patient via  
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
CC PTH-1/PTH-2 receptor agonists  
XX

Sequence 9 AA:

Query Match 52.7%; Score 37; DB 3; Length 9;  
Best Local Similarity 77.8%; Pred. No. 1.4e+06;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9  
Db 1 AVSEIQLMH 9

Search completed: May 18, 2004, 10:01:53  
Job time : 46.75 secs

Tue May 18 12:03:00 2004

us-09-730-174a-3.closed.rapb

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 10:04:51 ; Search time 33.25 Seconds  
(without alignments)  
100.425 Million cell updates/sec

Title: US-09-730-174A-3  
Perfect score: 59  
Sequence: 1 SVSEIQMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145566 segs, 278261457 residues  
Total number of hits satisfying chosen parameters: 166097

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10C\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	12	9	US-09-730-174A-3
2	56	94.9	12	9	US-09-730-174A-5
3	55	93.2	11	9	US-09-730-174A-1
4	55	93.2	12	9	US-09-730-174A-4
5	52	88.1	12	9	US-09-730-174A-6
6	51	86.4	11	9	US-09-730-174A-2
7	49	83.1	10	14	US-10-168-185-1
8	45	76.3	9	14	US-10-168-185-7
9	43	72.9	9	14	US-10-168-185-2
10	41	69.5	8	14	US-10-168-185-8
11	40	67.8	9	14	US-10-192-673-6
12	37	62.7	9	14	US-10-192-673-7
13	35	59.3	8	14	US-10-168-185-3
14	33	55.9	9	14	US-10-192-673-10
15	30	50.8	7	14	US-10-168-185-4

16	30	50.8	9	14	US-10-192-673-8	Sequence 8, Appli
17	29	49.2	10	14	US-10-033-741-61	Sequence 61, Appli
18	28	47.5	9	9	US-09-746-945-6	Sequence 6, Appli
19	28	47.5	12	14	US-10-319-130-16	Sequence 16, Appli
20	26	44.1	6	14	US-10-168-185-5	Sequence 5, Appli
21	26	44.1	10	14	US-10-168-185-11	Sequence 11, Appli
22	25	42.4	11	12	US-09-747-287-185	Sequence 185, App
23	24	40.7	10	9	US-09-826-290-27	Sequence 27, Appli
24	24	40.7	10	16	US-10-264-309-369	Sequence 369, App
25	24	40.7	11	12	US-10-609-217-41	Sequence 41, Appli
26	24	40.7	11	12	US-10-632-388-41	Sequence 41, Appli
27	24	40.7	11	12	US-10-651-723-41	Sequence 41, Appli
28	24	40.7	11	12	US-10-645-761-41	Sequence 41, Appli
29	24	40.7	11	16	US-10-666-696-41	Sequence 41, Appli
30	24	40.7	11	16	US-10-653-048-41	Sequence 41, Appli
31	24	40.7	12	14	US-10-286-457-234	Sequence 234, App
32	23	39.0	7	14	US-10-286-457-469	Sequence 469, App
33	23	39.0	7	15	US-10-368-280-12	Sequence 12, Appli
34	23	39.0	7	15	US-10-374-035-12	Sequence 12, Appli
35	23	39.0	9	9	US-09-894-018-332	Sequence 332, App
36	23	39.0	9	10	US-09-821-734-4	Sequence 4, Appli
37	23	39.0	9	10	US-09-854-248-11	Sequence 11, Appli
38	23	39.0	9	12	US-10-253-286-288	Sequence 288, App
39	23	39.0	9	14	US-10-094-699-50	Sequence 50, Appli
40	23	39.0	9	15	US-10-117-937-249	Sequence 249, App
41	23	39.0	9	15	US-10-245-871-288	Sequence 288, App
42	23	39.0	10	14	US-10-094-699-49	Sequence 49, Appli
43	23	39.0	10	15	US-10-026-066-31	Sequence 31, Appli
44	23	39.0	10	15	US-10-026-066-83	Sequence 83, Appli
45	23	39.0	10	15	US-10-117-937-248	Sequence 248, App

#### ALIGNMENTS

RESULT 1  
US-09-730-174A-3  
Sequence 3, Application US/09730174A  
Patent No. US20020110871A1  
GENERAL INFORMATION:  
APPLICANT: Zahradnik, R.J.  
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
FILE REFERENCE: IMMUNE-001A  
CURRENT APPLICATION NUMBER: US/09/730,174A  
CURRENT FILING DATE: 2000-12-05  
NUMBER OF SEQ ID NOS: 12  
SEQ ID NO 3  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
US-09-730-174A-3

Query Match 100.0%; Score 59; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00071;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SVSEIQMHNLG 12  
Db 1 SVSEIQMHNLG 12

RESULT 2  
US-09-730-174A-5  
Sequence 5, Application US/09730174A  
Patent No. US20020110871A1  
GENERAL INFORMATION:  
APPLICANT: Zahradnik, R.J.  
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
FILE REFERENCE: IMMUNE-001A  
CURRENT APPLICATION NUMBER: US/09/730,174A  
CURRENT FILING DATE: 2000-12-05  
NUMBER OF SEQ ID NOS: 12  
SEQ ID NO 3  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
US-09-730-174A-5

```

; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5
```

```

Query Match          94.9%; Score 56; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0024;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SVSEIQLMHNLG 12
        :|||||
Db       1 AVSEIQLMHNLG 12
```

```

RESULT 3
US-09-730-174A-1
; Sequence 1, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1
```

```

Query Match          93.2%; Score 55; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 VSEIQLMHNLG 12
        :|||||
Db       1 VSEIQLMHNLG 11
```

```

RESULT 4
US-09-730-174A-4
; Sequence 4, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4
```

```

Query Match          93.2%; Score 55; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      1 SVSEIQLMHNLG 12
        :|||||
Db       1 SVSEIQFMHNLG 12
```

```

RESULT 5
US-09-730-174A-6
; Sequence 6, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-6
```

```

Query Match          88.1%; Score 52; DB 9; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.012;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 SVSEIQLMHNLG 12
        :|||||
Db       1 AVSEIQFMHNLG 12
```

```

RESULT 6
US-09-730-174A-2
; Sequence 2, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-2
```

```

Query Match          86.4%; Score 51; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 VSEIQLMHNLG 12
        :|||||
Db       1 VSEIQFMHNLG 11
```

```

RESULT 7
US-10-166-185-1
; Sequence 1, Application US/10166185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Miesbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
```

```

; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-1

Query Match
Best Local Similarity 83.1%; Score 49; DB 14; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 SVSEIQLMHN 10
Db 1 SVSEIQLMHN 10
```

```

RESULT 8
US-10-168-185-7
; Sequence 7, Application US/10/168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-7

Query Match
Best Local Similarity 76.3%; Score 45; DB 14; Length 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 VSEIQLMHN 10
Db 1 VSEIQLMHN 9
```

```

RESULT 9
US-10-168-185-2
; Sequence 2, Application US/10/168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
```

```

; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-2
```

```

Query Match
Best Local Similarity 72.9%; Score 43; DB 14; Length 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 SVSEIQLMH 9
Db 1 SVSEIQLMH 9
```

```

RESULT 10
US-10-168-185-8
; Sequence 8, Application US/10/168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-8
```

```

Query Match
Best Local Similarity 69.5%; Score 41; DB 14; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 SEIQLMHN 10
Db 1 SEIQLMHN 8
```

```

RESULT 11
US-10-192-673-6
; Sequence 6, Application US/10/192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; FILE REFERENCE: 0609 4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
```

```

; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-192-673-6
```

```

Query Match          67.8%; Score 40; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SVSEIQLMH 9
        :|||||
Db       1 AVSEIQLMH 9
```

```

RESULT 12
US-10-192-673-7
; Sequence 7, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; FILE REFERENCE: 0609, 4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-192-673-7
```

```

Query Match          62.7%; Score 37; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SVSEIQLMH 9
        :|||||
Db       1 AVSEIQLMH 9
```

```

RESULT 13
US-10-168-185-3
; Sequence 3, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
```

```

; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-3
```

```

Query Match          59.3%; Score 35; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SVSEIQLMH 8
        :|||||
Db       1 SVSEIQLMH 8
```

```

RESULT 14
US-10-192-673-10
; Sequence 10, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; FILE REFERENCE: 0609, 4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-192-673-10
```

```

Query Match          55.9%; Score 33; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 SVSEIQLMH 9
        :|||||
Db       1 SVSEIQLMH 9
```

```

RESULT 15
US-10-168-185-4
; Sequence 4, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
```

; TITLE OF INVENTION: Activity in a Human Sample  
; FILE REFERENCE: HLZ-0040US  
; CURRENT APPLICATION NUMBER: US/10/168,185  
; CURRENT FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: PCT/EP00/12911  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: DE 19961350  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-168-185-4

Query Match 50.8%; Score 30; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQL 7  
Db 1 SVSEIQL 7

Search completed: May 18, 2004, 10:20:59  
Job time : 33.25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:58:45 ; Search time 12.75 Seconds  
(without alignments)  
48.589 Million cell updates/sec

Title: US-09-730-174A-3  
Perfect score: 59  
Sequence: 1 SVSEIQMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/prodata/2/1aa/PCUTS\_COMB.pep: \*  
6: /cgn2\_6/prodata/2/1aa/Backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	84.7	12	4	US-09-442-989-31
2	49	83.1	10	3	US-08-817-547A-1
3	43	72.9	9	3	US-08-817-547A-2
4	40	67.8	9	4	US-09-421-379-6
5	37	62.7	9	4	US-09-421-379-7
6	35	59.3	8	4	US-08-817-547A-3
7	33	55.9	9	4	US-09-421-379-10
8	32	54.2	11	6	5460978-3
9	30	50.8	7	3	US-08-817-547A-4
10	30	50.8	9	4	US-09-421-379-8
11	26	44.1	6	3	US-08-817-547A-5
12	26	44.1	10	2	US-08-428-257A-14
13	25	42.4	11	3	US-08-802-981-124
14	24	40.7	5	2	US-08-177-109A-56
15	24	40.7	5	2	US-08-687-706-56
16	24	40.7	5	3	US-08-817-547A-17
17	24	40.7	6	3	US-08-817-547A-16
18	24	40.7	7	3	US-08-817-547A-15
19	24	40.7	8	3	US-08-748-021-64
20	24	40.7	8	3	US-08-817-547A-14
21	24	40.7	8	3	US-08-974-297-64
22	24	40.7	9	3	US-08-817-547A-13
23	24	40.7	10	3	US-08-817-547A-7
24	24	40.7	11	3	US-08-726-464B-13
25	24	40.7	11	4	US-09-428-082B-41
26	23	39.0	7	4	US-09-336-093-12
27	23	39.0	7	4	US-09-557-465D-12

28	23	39.0	10	3	US-08-396-385-6	Sequence 6, Appl
29	23	39.0	10	4	US-09-287-221-6	Sequence 6, Appl
30	23	39.0	12	2	US-08-140-137A-42	Sequence 42, Appl
31	23	39.0	12	4	US-08-474-349A-271	Sequence 271, Appl
32	22	37.3	8	3	US-08-160-604-74	Sequence 74, Appl
33	22	37.3	8	3	US-08-160-604-75	Sequence 75, Appl
34	22	37.3	8	4	US-09-296-089-10	Sequence 10, Appl
35	22	37.3	8	4	US-09-551-976-10	Sequence 10, Appl
36	22	37.3	9	4	US-09-482-543-177	Sequence 177, App
37	22	37.3	10	2	US-08-248-839C-180	Sequence 180, App
38	22	37.3	11	3	US-08-160-604-73	Sequence 73, Appl
39	22	37.3	11	4	US-09-296-089-27	Sequence 27, Appl
40	22	37.3	11	4	US-08-475-955-56	Sequence 56, Appl
41	22	37.3	11	4	US-09-551-976-27	Sequence 27, Appl
42	22	37.3	12	4	US-09-690-454-89	Sequence 89, Appl
43	22	37.3	12	4	US-09-591-694-41	Sequence 41, Appl
44	21	35.6	5	3	US-08-817-547A-6	Sequence 6, Appl
45	21	35.6	6	2	US-08-621-803-184	Sequence 184, App

## ALIGNMENTS

RESULT 1  
US-09-442-989-31  
Sequence 31, Application US/09442989  
Patent No. 6569993  
GENERAL INFORMATION:  
APPLICANT: Sledeski, Adam W.  
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC  
FILE REFERENCE: A3113-US  
CURRENT APPLICATION NUMBER: US/09/442,989  
CURRENT FILING DATE: 1999-11-18  
EARLIER APPLICATION NUMBER: 60/081,897  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: Patentm Ver. 2.1  
SEQ ID NO 31  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)  
OTHER INFORMATION: FMOC-Ala  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (3)  
OTHER INFORMATION: Ser(OcBu)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (4)  
OTHER INFORMATION: Glu(OcBu)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (6)  
OTHER INFORMATION: Glu(Tyr)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (9)  
OTHER INFORMATION: His(Tyr)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (10)  
OTHER INFORMATION: Asn(Tyr)  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (8)  
OTHER INFORMATION: Nle  
US-09-442-989-31



Query Match 84.7% Score 50; DB 4; Length 12;  
Best Local Similarity 83.3%; Pred. No. 0.0045;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNIG 12  
Db 1 AVSEIQLMHNIG 12

RESULT 2  
US-08-817-547A-1  
Sequence 1, Application US/08817547A  
Patent No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Ademann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Magerlein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-817-547A-1

Query Match 83.1% Score 49; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0057;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHN 10  
Db 1 SVSEIQLMHN 10

RESULT 3  
US-08-817-547A-2  
Sequence 2, Application US/08817547A  
Patent No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Ademann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Magerlein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence

NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-817-547A-2

Query Match 72.9% Score 43; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9  
Db 1 SVSEIQLMH 9

RESULT 4  
US-09-421-379-6  
Sequence 6, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
FILE REFERENCE: 0609.4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: Peptide  
US-09-421-379-6

Query Match 67.8%; Score 40; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 3e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9  
DB 1 AVSEIQLMH 9

RESULT 5  
US-09-421-379-7  
Sequence 7, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
FILE REFERENCE: 0609.4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 7  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-421-379-7

Query Match 62.7%; Score 37; DB 4; Length 9;  
Best Local Similarity 77.8%; Pred. No. 3e+05;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9  
DB 1 AVSEIQLMH 9

RESULT 6  
US-08-817-547A-3  
Sequence 3, Application US/08817547A  
Patent No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Adermann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Magerlein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-817-547A-3

Query Match 59.3%; Score 35; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLM 8  
DB 1 SVSEIQLM 8

RESULT 7  
US-09-421-379-10  
Sequence 10, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
FILE REFERENCE: 0609.4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 10  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-421-379-10

Query Match 55.9%; Score 33; DB 4; Length 9;  
Best Local Similarity 77.8%; Pred. No. 3e+05;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9  
DB 1 SVSEIQLMH 9

RESULT 8  
5460978-3  
Patent No. 5460978  
APPLICANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,  
BRUCE E.; WETTERHALL, RICHARD E.H.  
TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL  
HYPERCALCEMIA OF MALIGNANCY-PTHrP

NUMBER OF SEQUENCES: 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/715,280  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 199,235  
FILING DATE: 09-MAY-1988  
APPLICATION NUMBER:  
FILING DATE:  
SEQ ID NO.3:  
LENGTH: 11  
5460978-3

Query Match 54.2%; Score 32; DB 6; Length 11;  
Best Local Similarity 70.0%; Pred. No. 8.2;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 1 SVSEIQLMHN 10  
Db 1 AVSEHQLEHN 10

RESULT 9  
US-08-817-547A-4

Sequence 4, Application US/08817547A

Patent No. 6030790

GENERAL INFORMATION:

APPLICANT: Adermann, Knut

APPLICANT: Hock, Dieter

APPLICANT: Magerlein, Markus

TITLE OF INVENTION: Peptides from the hPTH Sequence

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones & Askew, LLP

STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/817,547A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/03757

FILING DATE: 29 SEPT 1994

ATTORNEY/AGENT INFORMATION:

NAME: FROST, ROGER T.

REGISTRATION NUMBER: 22,176

REFERENCE/DOCKET NUMBER: 07826-0007

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-818-3700

TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: no

ANTI-SENSE: no

US-08-817-547A-4

Query Match 50.8%; Score 30; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SVSEIQL 7

Db 1 SVSEIQL 7

RESULT 10  
US-09-421-379-8

Sequence 8, Application US/09421379

Patent No. 6495662

GENERAL INFORMATION:

APPLICANT: Gardella, Thomas J.

APPLICANT: Kronenberg, Henry

APPLICANT: Potes, John T.

APPLICANT: Juppner, Harald

TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of

TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid

TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)

FILE REFERENCE: 0609,4570001

CURRENT APPLICATION NUMBER: US/09/421,379

CURRENT FILING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: U.S. 60/105,530

EARLIER FILING DATE: 1998-10-22

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 9

TYPE: PPT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-421-379-8

Query Match 50.8%; Score 30; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 0;

Cy 1 SVSEIQLMHN 9  
Db 1 AVSEHQLEHN 9

RESULT 11

US-08-817-547A-5

Sequence 5, Application US/08817547A

Patent No. 6030790

GENERAL INFORMATION:

APPLICANT: Adermann, Knut

APPLICANT: Hock, Dieter

TITLE OF INVENTION: Peptides from the hPTH Sequence

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones & Askew, LLP

STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/817,547A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/03757

FILING DATE: 29 SEPT 1994

ATTORNEY/AGENT INFORMATION:

NAME: FROST, ROGER T.

REGISTRATION NUMBER: 22,176

REFERENCE/DOCKET NUMBER: 07826-0007

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-817-547A-5

Query Match 44.1%; Score 26; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 SVSEIQ 6  
Db 1 SVSEIQ 6

RESULT 12  
US-08-428-257A-14  
Sequence 14, Application US/08428257A  
Patent No. 5865808  
GENERAL INFORMATION:  
APPLICANT: Spooner, Robert A.  
APPLICANT: Epenetos, A. A.  
TITLE OF INVENTION: Compounds to target cells  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jules E. Goldberg  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10016-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,257A  
FILING DATE: 07/05/95  
CLASSIFICATION: 514  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-428-257A-14

Query Match 44.1%; Score 26; DB 2; Length 10;  
Best Local Similarity 71.4%; Pred. No. 94; Indels 0; Gaps 0;  
Matches 5; Conservative 2; Mismatches 0;

QY 1 SVSEIOL 7  
Db 3 TVSEVOL 9

RESULT 13  
US-08-802-981-124  
Sequence 124, Application US/08802981  
Patent No. 6037137  
GENERAL INFORMATION:  
APPLICANT: Komoriya, Akira  
APPLICANT: Packard, Beverly S.  
TITLE OF INVENTION: Compositions for the Detection of Enzyme

TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof  
NUMBER OF SEQUENCES: 231  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 016865-000300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /product= "Aib"  
US-08-802-981-124

Query Match 42.4%; Score 25; DB 3; Length 11;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0;

QY 6 QLMHN 10  
Db 5 QLMHN 9

RESULT 14  
US-08-177-109A-56  
Sequence 56, Application US/08177109A  
Patent No. 5865615  
GENERAL INFORMATION:  
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby  
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Padst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30308-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/177,109A  
FILING DATE: 03-JAN-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:

Tue May 18 12:02:59 2004

us-09-730-174a-3.closed.rai

Page 6

NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: WU 107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-177-109a-56

Query Match 40.7%; Score 24; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MNLG 12  
:|:|  
Db 1 LNMWG 5

RESULT 15  
US-08-687-706-56  
Sequence 56, Application US/08687706  
Patent No. 5828892  
GENERAL INFORMATION:  
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby  
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,706  
FILING DATE: 26-JUL-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/177,109  
FILING DATE: 03-JAN-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: WU 107 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-687-706-56

Query Match 40.7%; Score 24; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MNLG 12  
:|:|  
Db 1 LNMWG 5

Search completed: May 18, 2004, 10:06:43  
Job time: 12.75 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: May 18, 2004, 09:56:10 ; Search time 10.25 Seconds  
(without alignments)

112.614 Million cell updates/sec

Title: US-09-730-174a-4  
Perfect score: 61  
Sequence: 1 SVSEIQFMNIG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	23	37.7	10	2	S28055	cytochrome b559 co
2	18	29.5	7	2	A58718	carotenoid U149 - Ca
3	18	29.5	9	2	S78420	ribosomal protein
4	18	29.5	10	2	A60589	spectrin-activating p
5	17	27.9	8	2	A05169	neuropeptide M-I -
6	17	27.9	10	2	A37268	IG heavy chain C r
7	17	27.9	12	2	S21205	IG heavy chain V r
8	17	27.9	12	2	PH1187	T-cell receptor al
9	16	26.2	7	2	A46868	alpha-myosin heavy
10	16	26.2	9	2	G58502	kidney and bladder
11	16	26.2	10	2	UC1416	hypertrehalosemic
12	16	26.2	10	2	S09138	hypertrehalosemic
13	16	26.2	11	2	A32428	amine oxidase (cop
14	15	24.6	7	2	S29735	polyphosphate-gluc
15	15	24.6	9	2	PT0231	IG heavy chain CDR
16	15	24.6	9	2	A56029	N-methylpurine DNA
17	15	24.6	10	2	S33844	alpha-2-macroglobu
18	15	24.6	10	2	S27873	hypothetical prote
19	15	24.6	10	2	S38304	lectin GNL1 alpha
20	15	24.6	11	2	A38841	rhodopsin homolog
21	15	24.6	11	2	S35490	type II site-speci
22	15	24.6	12	2	PH1190	T-cell receptor al
23	15	23.0	4	2	A51737	T-cell receptor be
24	14	23.0	7	2	A35779	neuropeptide Antho
25	14	23.0	7	2	UN0859	peptidyl-dipeptida
26	14	23.0	7	2	S78024	ribosomal protein
27	14	23.0	8	2	S08995	hypertrehalosemic
28	14	23.0	8	2	A49823	adipokinetic hormo
29	14	23.0	8	2	A44960	neuropeptide led-C

30	14	23.0	9	2	PM0002	chlorophyll a/b-bi
31	14	23.0	9	2	S13636	coat protein beta
32	14	23.0	9	2	PM0238	IG heavy chain CRD
33	14	23.0	10	1	SEPGNK	neuremedin K - pig
34	14	23.0	10	2	C61033	lanatACHXinin C -
35	14	23.0	10	2	B46453	e antigen p20 pre
36	14	23.0	10	2	S70251	nitrogenase (EC 1.
37	14	23.0	11	2	B41835	translacton elonga
38	14	23.0	11	2	S19301	endo-1,4-beta-xyla
39	14	23.0	11	2	PM0028	protein OA100042 -
40	14	23.0	11	2	SE0354	retinal oxidase -
41	14	23.0	11	2	S53456	beta-D-galactosida
42	14	23.0	11	2	PM0904	T-cell receptor be
43	14	23.0	12	1	A43975	locustamyotropin -
44	14	23.0	12	2	S25485	transcription fact
45	14	23.0	12	2	S71034	potB protein - Sal

## ALIGNMENTS

## RESULT 1

S28055

cytochrome b559 component psbf - pepper chloroplast (fragment)

C/Species: chloroplast Capsicum annuum (pepper)

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-Jun-1999

C/Accession: S28055

R/Kurtz, M.; Camara, B.; Weill, J.H.; Schantz, R.

Plant Mol. Biol. 20, 1185-1188, 1992

A/Title: The psbL gene from bell pepper (Capsicum annuum): plastid RNA editing also occu

A/Reference number: S28055, MUID:93099270, PMID:1463853

A/Accession: S28055

A/Molecule type: DNA

A/Residues: 1-10 <KUN>

A/Cross-references: EMBL:X65570; NID:G14344; PIDN:CAA46539.1; PID:G415734

A/Genes: psbf

A/Genome: chloroplast

A/Superfamily: cytochrome b559 component F

C/Keywords: chloroplast, photosynthesis, photosystem II, chlaxoid

## Query Match

Best Local Similarity 37.7%; Score 23; DB 2; Length 10;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY

DB

1 SVSEIQFM 8

1 SISAWQFI 8

## RESULT 2

A58718

carotenoid U149 - Carnobacterium sp. (fragment)

C/Species: Carnobacterium sp.

C/Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998

C/Accession: A58718

R/Stocfefs, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.

Appl. Environ. Microbiol. 58, 1417-1422, 1992

A/Title: Purification and characterization of a new bacteriocin isolated from a Carnobac

A/Reference number: A58718, MUID:92321768, PMID:162206

A/Accession: A58718

A/Status: preliminary

A/Molecule type: Protein

A/Residues: 1-7 <STO>

C/Keywords: antibiotic, lanthionine

## Query Match

Best Local Similarity 29.5%; Score 18; DB 2; Length 7;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

DB

3 SEIQ 6

2 SEIQ 5

RESULT 3  
S78420  
ribosomal protein RL41, mitochondrial [validated] - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000  
C/Accession: S78420  
R/Goldschmidt-Reisin, S.; Graack, H.R.  
submitted to the Protein Sequence Database, February 1998  
A/Reference number: S78411  
A/Accession: S78420  
A/Molecule type: protein  
A/Residues: 1-9 <GOL>  
A/Note: the protein is designated as mitochondrial ribosomal protein L41  
C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 29.5%; Score 18; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12  
: |||  
Db 5 HRLG 8

RESULT 4  
A60589  
sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchin  
C/Species: Heterocentrotus mamillatus  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
C/Accession: A60589  
R/Ishino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, Y.  
Comp. Biochem. Physiol. B 94, 739-751, 1989  
A/Title: A halogenated amino acid-containing sperm activating peptide and its related peptidase  
A/Reference number: A60527  
A/Accession: A60589  
A/Molecule type: protein  
A/Residues: 1-10 <YOS>  
C/Keywords: unassigned animal peptides

Query Match 29.5%; Score 18; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 2e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNLG 12  
: |||  
Db 2 YNLG 5

RESULT 5  
A05169  
neuropeptide M-I - American cockroach  
C/Species: Periplaneta americana (American cockroach)  
C/Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Dec-1993  
C/Accession: A05169  
R/Willem, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.  
Biochem. Biophys. Res. Commun. 124, 350-358, 1984  
A/Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry  
A/Reference number: A90118; MUID:85046530; PMID:6548628  
A/Accession: A05169  
A/Molecule type: protein  
A/Residues: 1-8 <MIT>  
C/Keywords: neuropeptide

Query Match 27.9%; Score 17; DB 2; Length 8;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 EIQFMHN 10  
: |||  
Db 1 EVNFSN 7

RESULT 6  
A37268  
Ig heavy chain C region (I29) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998  
C/Accession: A37268  
R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glanney Jr., J.R.  
J. Biol. Chem. 266, 6607-6613, 1991  
A/Title: Heavy and light chain variable region sequences and antibody properties of anti-  
A/Reference number: A3740; MUID:91177923; PMID:1706720  
A/Accession: A37268  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-10 <RUF>

Query Match 27.9%; Score 17; DB 2; Length 10;  
Best Local Similarity 44.4%; Pred. No. 3.1e+05;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMHN 12  
: |||  
Db 1 ESQSFN 9

RESULT 7  
S21205  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C/Accession: S21205  
R/Makiya, R.; Stigbrand, T.  
Eur. J. Biochem. 205, 341-345, 1992  
A/Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin-C  
A/Reference number: S21205; MUID:92209522; PMID:1555592  
A/Accession: S21205  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12 <MAK>  
C/Keywords: heterotetramer; immunoglobulin

Query Match 27.9%; Score 17; DB 2; Length 12;  
Best Local Similarity 33.3%; Pred. No. 3.8e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 EIQFMHN 12  
: |||  
Db 1 EVOLVSG 9

RESULT 8  
PH187  
T-cell receptor alpha chain V region (Cw3/1P1) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH187  
R/Casanova, J.L.; Cecottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wild  
J. Exp. Med. 176, 439-447, 1992  
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A/Reference number: S6512; MUID:92364546; PMID:1380061  
A/Accession: PH187  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-12 <CAS>

Query Match 27.9%; Score 17; DB 2; Length 12;  
Best Local Similarity 57.1%; Pred. No. 3.8e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIOF 7  
: |||  
Db 2 AVSEIOF 8

RESULT 9  
146868  
alpha-myosin heavy chain - rabbit (fragment)  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 05-Nov-1999  
C/Accession: 146868  
R.Friedman, D.J.; Umada, P.K.; Sinha, A.M.; Hsu, H.  
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984  
A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricular  
A/Reference number: 146868; MUID:84221901; PMID:6328491  
A/Accession: 146868  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-7 <FRT>  
A/Cross-references: GB:K01698; NID:9165538; PID:NAA31415.1; PID:9165539

Query Match  
Best Local Similarity 26.2%; Score 16; DB 2; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QFMNH 10  
| : | : | :  
1 QFMNH 5

Db 1 QFMNH 5

RESULT 10  
G58502  
kidney and bladder stone protein - unidentified bacterium (fragment)  
C/Species: unidentified bacterium  
C/Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C/Accession: G58502  
R.Binet, J.P.; Binette, M.B.  
Submitted to the Protein Sequence Database, October 1996  
A/Description: The proteins of kidney and gallbladder stones.  
A/Reference number: A58501  
A/Accession: G58502  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <BIN>  
A/Experimental source: human kidney stone, bladder stone  
A/Note: a secondary sequence AAKENPKD was also found

Query Match  
Best Local Similarity 26.2%; Score 16; DB 2; Length 9;  
Best Local Similarity 28.6%; Pred. No. 2.8e+05;  
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYSEIOF 7  
| : | : | :  
1 SLDPVXF 7

Db 1 SLDPVXF 7

RESULT 11  
JC1416  
hypertrehalosemic hormone I - stick insect (Carausius morosus)  
N/Alternate names: neuropeptide Cam-HrTH-I  
N/contains: hypertrehalosemic factor II  
C/Species: Carausius morosus  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: JC1416; S07157  
R.Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.  
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992  
A/Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick in  
A/Reference number: JC1416; MUID:93129188; PMID:1482345  
A/Accession: JC1416  
A/Molecule type: protein  
A/Residues: 1-10 <GAE1>  
R.Gaede, G.; Rinehart Jr., K.L.  
Biol. Chem. Hoppe-Seyler 368, 67-75, 1987  
A/Title: Primary structure of the hypertrehalosemic factor II from the corpus cardiacum  
A/Reference number: S07157; MUID:87157103; PMID:3828078  
A/Accession: S07157

A/Molecule type: protein  
A/Residues: '2', 2-10 <GAE2>  
C/Comment: Hypertrehalosemic factor II lacks the tryptophan modification.  
C/Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplanet  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic ac  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/8/Binding site: carboxylate (Tyr) (covalent) #status experimental  
F/10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match  
Best Local Similarity 26.2%; Score 16; DB 2; Length 10;  
Best Local Similarity 33.3%; Pred. No. 4.8e+03;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMNLG 12  
| : | : | :  
1 QLFTFPMWG 9

Db 1 QLFTFPMWG 9

RESULT 12  
S09138  
hypertrehalosemic hormone II - stick insect (Exotosoma tiaratum)  
N/Alternate names: Cam-HrTH-II  
C/Species: Exotosoma tiaratum  
C/Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997  
C/Accession: S09138  
R.Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpor  
entalis and of the stick insect Exotosoma tiaratum assigned by tandem fast atom bombard  
A/Reference number: S08995; MUID:90253659; PMID:2340112  
A/Accession: S09138  
A/Molecule type: protein  
A/Residues: 1-10 <GAE>  
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match  
Best Local Similarity 26.2%; Score 16; DB 2; Length 10;  
Best Local Similarity 33.3%; Pred. No. 4.8e+03;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMNLG 12  
| : | : | :  
1 QLFTFPMWG 9

Db 1 QLFTFPMWG 9

RESULT 13  
A32428  
amine oxidase (copper-containing) (EC 1.4.3.6) - pig (fragment)  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 12-Oct-1989 #sequence\_revision 31-Dec-1993 #text\_change 06-Sep-1996  
C/Accession: A32428  
R.van der Meer, R.A.; Van Wassenar, P.D.; Van Brouwerhaven, J.H.; Duine, J.A.  
Biochem. Biophys. Res. Commun. 159, 726-733, 1989  
A/Title: Primary structure of a pyrroloquinoline quinone (PQQ) containing peptide isolat  
A/Reference number: A32428; MUID:89193662; PMID:2539124  
A/Accession: A32428  
A/Molecule type: protein  
A/Residues: 1-7, 'K', 9-11 <VAN>  
A/Note: the modified residue thought by the authors to be pyrroloquinoline quinone cov  
C/Keywords: oxidoreductase; quinoprotein; topaquinone  
F/10/Modified site: topaquinone (Tyr) #status predicted

Query Match  
Best Local Similarity 26.2%; Score 16; DB 2; Length 11;  
Best Local Similarity 37.5%; Pred. No. 5.3e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 SEIQFMNH 10  
| : | : | :  
2 SDAVFYTN 9



Tue May 18 12:03:04 2004

us-09-730-174a-4.closed.rpr

Page 4

RESULT 14

S29735  
Polyphosphate-glucose phosphotransferase (EC 2.7.1.63) - *Propionibacterium freudenreichii*  
C:Species: *Propionibacterium freudenreichii* subsp. *shermanii*  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 03-Jun-2002  
C/Accession: S29735  
R:Phillips, N.F.B.; Horn, P.J.; Wood, H.G.  
Arch. Biochem. Biophys. 300, 309-319, 1993  
A:Title: The polyphosphate- and ATP-dependent glucokinase from *Propionibacterium shermanii*  
A/Reference number: S29735; MUID:9314332; PMID:8380966  
A/Accession: S29735  
A>Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <PHI>  
C:Keywords: phosphotransferase

Query Match 24.6%; Score 15; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 HNLG 12  
| | |  
Db 2 HVLG 5

RESULT 15

PT0231  
Ig heavy chain CDR3 region (clone 1-118B) - human (fragment)  
C:Species: *Homo sapiens* (man)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0231  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A/Reference number: PT0222; MUID:9108337; PMID:1899102  
A/Accession: PT0231  
A/Molecule type: DNA  
A/Residues: 1-9 <IAM>  
A/Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 24.6%; Score 15; DB 2; Length 9;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 7 FMHNLG 12  
: | : |  
Db 1 YTHSEG 6

Search completed: May 18, 2004, 10:05:40  
Job time : 10.25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:43:45 ; Search time 6.75 Seconds  
(without alignments)  
92.569 Million cell updates/sec

Title: US-09-730-174A-4  
Perfect score: 61  
Sequence: 1 SVSEIQTQFMHNG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	23	37.7	10 1 PSBF_CAPAN	O03367 capsicum an
2	18	29.5	7 1 LANC_CARUT	P36860 carnobacter
3	18	29.5	10 1 HTP1_ROMMT	P18110 romalea mic
4	16	26.2	8 1 ALI6_CYPDO	P82157 cydia pomon
5	16	26.2	10 1 HTP2_CARMO	P11385 carausius m
6	15	24.6	5 1 EIO3_LITRU	P82099 litorea rub
7	15	24.6	8 1 FUS8_FUSCO	P81010 fusarium so
8	15	24.6	10 1 RRP1_PHOVS	P35846 phocine dis
9	15	24.6	11 1 BRG_CLOPA	P81350 clostridium
10	15	24.6	11 1 NUH1_CANFA	P49820 canis fam11
11	15	24.6	11 1 T2P1_PROVU	P31031 proteus vul
12	14	23.0	4 1 FLRN_ANTEP	P58707 anthopleura
13	14	23.0	7 1 ALI7_CYPDO	P82158 cydia pomon
14	14	23.0	7 1 TV51_LITRU	P82065 litorea rub
15	14	23.0	8 1 ALI8_CARMA	P81821 carcinus ma
16	14	23.0	8 1 ALI1_CYPDO	P82152 cydia pomon
17	14	23.0	8 1 HTP1_PERAM	P04548 periplaneta
18	14	23.0	9 1 FAR8_MACRS	P83181 macrobrachi
19	14	23.0	9 1 UF02_MOUSE	P38640 mus musculu
20	14	23.0	10 1 ALI9_CARMA	P81822 carcinus ma
21	14	23.0	10 1 TRNC_PANCA	P22690 rana catesb
22	14	23.0	10 1 TRNC_PANCA	P01392 sus scrofa
23	14	23.0	11 1 ASL1_BACSE	P83146 bacteroides
24	14	23.0	12 1 HCV1_CARMA	P83176 carcinus ma
25	14	23.0	12 1 LMT1_LOCOMI	P22395 locusta mig
26	14	23.0	12 1 FOR2_METIM	P80903 mehandact
27	14	23.0	12 1 RS19_TOBBP	O56251 tomato big
28	13	21.3	6 1 TRP1_PSEBP	P36414 pseudomonas
29	13	21.3	8 1 HTP1_TENNO	P25519 tenebrio mo
30	13	21.3	8 1 LCK4_LEUMA	P21143 leucophaea
31	13	21.3	8 1 LCK6_LEUMA	P19988 leucophaea
32	13	21.3	9 1 CONO_CONGE	P05486 conus geogr
33	13	21.3	9 1 MOSH_CLYJA	P19952 clypeaster

34	13	21.3	9 1 OXYT_EISFO	P42998 eisenia foe
35	13	21.3	9 1 PPX1_PERAM	P82691 periplaneta
36	13	21.3	11 1 ASL2_BACSE	P83147 bacteroides
37	13	21.3	11 1 COR2_PERAM	P11495 periplaneta
38	13	21.3	11 1 CSIS_BACSU	P81095 bacillus su
39	13	21.3	11 1 PVK1_PERAM	P41837 periplaneta
40	13	21.3	11 1 O2O3_COMTE	P80464 comamonas t
41	13	21.3	12 1 UKA2_ROMAN	P31144 homo sapien
42	13	21.3	12 1 UR2_POLSP	P81022 poliodon sp
43	12	19.7	5 1 RE21_LITRU	P82071 litorea rub
44	12	19.7	5 1 RE31_LITRU	P82072 litorea rub
45	12	19.7	8 1 ANG2_BOTJA	Q10582 boehrops ja

## ALIGNMENTS

## RESULT 1

PSBF\_CAPAN STANDARD; PRT; 10 AA.

ID	PSBF_CAPAN	STANDARD	PRT	10 AA.
AC	O03367			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Cytochrome b559 beta subunit (PSII reaction center subunit VI)			
DE	(Fragment).			
GN	PSBF			
OS	Capsicum annuum (Bell pepper).			
OC	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Lamiales; Solanales; Solanaceae; Capsicum.			
OX	NCBI_TaxID=4072.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Lamuyo; TISSUE=fruit, and leaf;			
RX	MEDLINE=93099270; PubMed=1463853;			
PA	Kuntz M., Camara B., Weil J.-H., Schantz R.;			
RT	"The psbL gene from bell pepper (Capsicum annuum): placid RNA			
RT	editing also occurs in non-photosynthetic chromoplasts. "			
RL	Plant Mol. Biol. 20:1185-1188(1992).			
CC	-!- FUNCTION: This b-type cytochrome is tightly associated with the			
CC	reaction center of photosystem II and possibly is part of the			
CC	water-oxidation complex.			
CC	-!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.			
CC	-!- SIMILARITY: Belongs to the psbL / psbF family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; X65570; CAA46539.1; ..			
DR	PIR; S28055; S28055.			
DR	HAMAP; MF_00643; -? 1.			
DR	InterPro; IPR006216; Cyt_b559.			
DR	PROSITE; PS00537; CYTOCHROME B559; PARTIAL.			
KW	Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.			
FT	NON TER			
FT	TRANSMEM			
FT	DOMAIN			
SQ	SEQUENCE 10 AA; 1180 MW; 817D0F59D6D6DCS CRC64;			
BY	SIMILARITY.			
LEWENAL (POTENTIAL).				
Query Match	37.7%; Score 23; DB 1; Length 10;			
Best Local Similarity	50.0%; Pred. No. 1.2e+02;			
Matches	4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;			
OY	1 SVSEIQTQFM 8			
DB	1 SISAMQPI 8			

```
RESULT 2
LANC_CARUI STANDARD; PRT; 7 AA.
ID LANC_CARUI
AC P36960;
DT 01-JUN-1994 (Rel. 28, Created)
DT 01-JUN-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lanthibiotic caruocin U149 (Fragment).
OS Carnobacterium sp. (strain U149).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
CC Carnobacterium.
NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -1- FUNCTION: Lanthionine-containing peptide antibiotic (lanthibiotic).
KW Antibiotic; Bacteriocin; Lanthibiotic.
FT NON TER
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 29.5%; Score 18; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIO 6
DB 2 SEIO 5

RESULT 3
HTF1_ROMMI STANDARD; PRT; 10 AA.
ID HTF1_ROMMI
AC P11810;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RO I (Hypertrehaloseamic factor).
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
CC Acridoidea; Romaleidae; Romalea.
NCBI_TaxID=7007;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226949;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the ACH/RFCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -1- FUNCTION: Hypertrehaloseamic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the ACH / RFCH / RFCH family.
DR InterPro; IPR002047; ACH.
DR PROSITE; PS00256; ACH; 1.
KW Neuropeptide; Amidation; flight; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1163 MW; 056236745711A9C4 CRC64;

Query Match 29.5%; Score 18; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 4 EIOFMHNG 12
DB 1 QVNFTRNG 9

RESULT 4
AL6_CYPDO STANDARD; PRT; 8 AA.
ID AL6_CYPDO
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydia pomonella (Codling moth).
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RX TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Davey H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 26.2%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 HENIG 12
DB 3 LYNFG 7

RESULT 5
HTF2_CARMO STANDARD; PRT; 10 AA.
ID HTF2_CARMO
AC P1185;
DT 01-JUL-1999 (Rel. 11, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehaloseamic factor II (HTF-II) (HRT-II) (Hypertrehaloseamic
DE neuropeptide II).
OS Carausius morosus (Indian stick insect), and
OS Extalosoma tiaratum (Stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatodea;
CC Euphasmida; Carausius.
NCBI_TaxID=7022, 7024;
RN [1]
RP SEQUENCE.
RX SPECIES=C. morosus; TISSUE=Corpora cardiaca;
RX MEDLINE=87157103; PubMed=3828078;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structure of the hypertrehaloseamic factor II from the
RT corpus cardiaca of the Indian stick insect, Carausius morosus,
RT determined by fast atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN [2]
RP SEQUENCE.
RX SPECIES=E. tiaratum; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehaloseamic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Grylloblatta campodeiformis, and Blattella germanica and Blattella orientalis
```

```

RT and of the stick insect Extracoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RC CARBOHYDRATE-LINKAGE SITE.
RC SPECIES=C. morosus; TISSUE=corpora cardiaca;
RX MEDLINE=91129188; PubMed=1482345.
RA Gaede G., Keilner R., Rinehart K.L. Jr., Proefke M.L.;
RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC -1- FUNCTION: Hyperrealease factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1308.61; METHOD=FAH.
CC -1- SIMILARITY: Belongs to the AKH / HPTH / RPCH family.
DR PIR: J01416; J01416.
DR PIR: S09138; S09138.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Analation; Glycoprotein; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A5D1 CRC64;

Query Match 26.2%; Score 16; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 2.7e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 4 EIOFMHNLG 12
DB 1 QLTFTPNWG 9

RESULT 6
EIO3 LITRU STANDARD; PRT; 5 AA.
AC P82059;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eumelestomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OC NCB1_TaxID=104895;
RN [1]
RP SEQUENCE.
RP TISSUE=Skin secretion;
RA Mahnir P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RL rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A0000 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FMH 9
DB 1 FVH 3

RESULT 7

```

```

FUSS_FUSSO STANDARD; PRT; 8 AA.
ID FUSS_FUSSO
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Allergen Fus 8 13596* (Fragment).
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCB1_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma V., Gangal S.V.;
RL Submitted (JUL-1997) to Swiss-Prot.
CC -1- ALLERGEN: Causes an allergic reaction in human.
KW Allergen.
FT NON_TER 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 HNL 11
DB 5 HNV 7

RESULT 8
ID RPPL_PRODV STANDARD; PRT; 10 AA.
AC P35946;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (large structural protein)
DE (L protein) (Fragment).
GN L.
OS Phocine distemper virus (PDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCB1_TaxID=11240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U1stref/89;
RX MEDLINE=92268877; PubMed=1588321;
RA Curran M.D., O'Loan D., Kennedy S., Rima B.K.;
RT "Molecular characterization of phocine distemper virus: gene order
RT and sequence of the gene encoding the attachment (H) protein."
J. Gen. Virol. 73:1189-1194(1992).
CC -1- FUNCTION: Probable component of the active polymerase. It may
CC function in mRNA synthesis, capping, methylation and poly(A)
CC synthesis of newly synthesized viral mRNAs. RNA editing of the P
CC gene transcript, and protein kinase activity.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate +
CC {RNA} (N).
CC -1- SIMILARITY: Belongs to the paramyxoviruses L protein family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D10371; BAA01208.1; -
KW Transferase; RNA-directed RNA polymerase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;

```

```

Query Match      24.6%; Score 15; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEI 5
   ||:|
   5 SVN01 9

Db

RESULT 9
EFG_CLOPA STANDARD; PRT; 11 AA.
ID EFG_CLOPA
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUS1.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=MS;
RX MEDLINE=98291870; PubMed=9629918;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum MS.";
RI Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
the nascent protein chain from the A-site to the P-site of the
ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro: IPR000795; EF_Grpbind.
DR PROSITE: PS00301; EFACOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
RN NON_TER 11
SQ SEQUENCE 11 AA; 1337 MW; 412E72F1D9C33B17 CRC64;

Query Match      24.6%; Score 15; DB 1; Length 11;
Best Local Similarity 25.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 IQFMHNLG 12
   ||:|
   4 LEKFNQIG 11

Db

RESULT 10
NDHM_CANPA STANDARD; PRT; 11 AA.
ID NDHM_CANPA
AC P49820;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Fragment).
GN NDUFV2.
OS Caris familiaris (Dog).
OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RI Electrophoresis 18:2795-2802(1997).

```

```

CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FS)
FRAGMENT OF THE ENZYME.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COFACTOR: Binds 1 2Fe-2S cluster (potential).
CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
DR HSC-2DPAGE; P49820; DOG.
DR InterPro: IPR002023; Cmplx1_24kDa.
DR PROSITE: PS01099; COMPLEX1_24K; PARTIAL.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
KW Iron-sulfur; Iron; 2Fe-2S.
RN NON_TER 11
SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match      24.6%; Score 15; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.7e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FVH 9
   ||:|
   7 FVH 9

Db

RESULT 11
T2P1_PROVU STANDARD; PRT; 11 AA.
ID T2P1_PROVU
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Type II restriction enzyme PvuII (EC 3.1.21.4) (Endonuclease PvuII)
DE (R.PvuII) (Fragment).
GN PvuII.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13315;
RX MEDLINE=93087186; PubMed=1454536;
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvuII restriction and
RT modification system.";
RI Nucleic Acids Res. 20:5743-5747(1992).
CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CLEAVES AFTER T-4.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
specific double-stranded fragments with terminal 5'-phosphates.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L04163; AAA25660.1; -.
DR PIR: S35490; S35490.
DR REBASE: 1541; PvuII.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
RN NON_TER 1
SQ SEQUENCE 11 AA; 1300 MW; 9FCDE7955B72B1A CRC64;

Query Match      24.6%; Score 15; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 SYSEI 5  
| | |  
DB 2 SYDEL 6

## RESULT 12

FLRN ANTEL STANDARD; PRT; 4 AA.  
ID FLRN ANTEL  
AC P58707;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Antho-RNamide.  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;  
OC Nymathea; Actinellidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RX MEDLINE=90319122; PubMed=1973541;  
RA Grimmelikhuijsen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,  
RA Reischneider R.K., Nohacker H.-P., Staley A.L.;  
RT "Isolation of L-3-phenylalanyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea  
RT anemone neuropeptide containing an unusual amino-terminal blocking  
RT group.";  
RT Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).  
RL -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Neuron specific.  
CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.  
DR PIR: A35779; A35779.  
KM Neuropeptide; Amidation.  
FT MOD\_RES 1 4 L-3-PHENYLALANYL.  
FT MOD\_RES 1 1 AMIDATION.  
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 EHEM 10  
| | |  
DB 1 FLRN 4

RESULT 13  
ALL7\_CYPDPO STANDARD; PRT; 7 AA.  
ID ALL7\_CYPDPO  
AC P82158;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydiastatin 7.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily.";  
RL Peptides 18:1301-1309(1997).  
CC -1- SIMILARITY: Belongs to the allatostatin family.  
KM Neuropeptide; Amidation.  
FT MOD\_RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 873 MW; 672879CAB8569350 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 7;  
Best Local Similarity 40.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 8 MENLG 12  
| | |  
DB 2 MIDFG 6

## RESULT 14

TY51 LITRU STANDARD; PRT; 7 AA.  
ID TY51 LITRU  
AC P82065;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tytophyllin 5.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion.  
RA Seibomner S.T., Mabiniz P.A., Maugh R.J., Bowie J.R., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog  
RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
RT of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
CC -1- MASS SPECTROMETRY: MW=965; METHOD=FAB.  
KM Amphibian defense peptide; Amidation; Neuropeptide;  
KM Pyrolidone carboxylic acid.  
FT MOD\_RES 1 7 PYROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 1 7 AMIDATION.  
SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 7;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 EIOFMH 9  
| | |  
DB 1 QIPWFH 6

RESULT 15  
AL18 CARVA STANDARD; PRT; 8 AA.  
ID AL18 CARVA  
AC P81821;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 18.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jarois P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.  
CC -1- SIMILARITY: Belongs to the allatostatin family.  
KM Neuropeptide; Amidation; Multigene family.

FT MOD RES 8 8 AMIDATION (POTENTIAL).  
 SQ SEQUENCE 8 AA; 919 MW; C82879D5A569AB5 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 8 MHNLG 12  
 |::|  
 Db 3 MYSFG 7

Search completed: May 18, 2004, 10:02:34  
 Job time : 7.75 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: May 18, 2004, 09:55:20 ; Search time 30.25 Seconds

(without alignments)  
125.164 Million cell updates/sec

Title: US-09-730-174A-4

Perfect score: 61

Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL\_25: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mmc: \*  
8: sp\_organelle: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_virus: \*  
16: sp\_bacteriophage: \*  
17: sp\_archaeophages: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	39.3	11	13 Q9PS71	Q9PS71 Agkistrodon
2	19	31.1	8	6 Q9TT78	Q9TT78 canis fam1
3	19	31.1	9	12 Q92766	Q92766 canine dist
4	19	31.1	9	12 Q71066	Q71066 canine dist
5	19	31.1	12	13 P82081	P82081 limodyst
6	18	29.5	8	3 Q13591	Q13591 saccharomyc
7	18	29.5	10	4 Q15342	Q15342 homo sapien
8	18	29.5	12	8 Q8E850	Q8E850 anoda crist
9	18	29.5	12	15 Q85631	Q85631 avian carc1
10	17	27.9	11	5 Q23876	Q23876 dictyostel
11	17	27.9	11	8 Q35374	Q35374 paramesum
12	16	26.2	7	6 Q28742	Q28742 oryctolagus
13	16	26.2	7	13 Q84J20	Q84J20 gallus gall
14	16	26.2	8	3 Q05403	Q05403 saccharomyc
15	16	26.2	8	10 Q40659	Q40659 oryza sativ
16	16	26.2	8	13 P82082	P82082 limodyst

17	16	26.2	8	13 P82083	P82083 limodyst
18	16	26.2	9	2 Q44377	Q44377 aeromonas t
19	16	26.2	9	2 Q44468	Q44468 aeromonas v
20	16	26.2	9	2 Q8RKU3	Q8RKU3 borrelia bu
21	16	26.2	9	2 Q43928	Q43928 aeromonas p
22	16	26.2	9	2 Q44001	Q44001 aeromonas e
23	16	26.2	9	10 Q9FX10	Q9FX10 l11ium long
24	16	26.2	11	8 Q9GB68	Q9GB68 elaeis guin
25	16	26.2	11	10 P82336	P82336 pistum sativ
26	16	26.2	12	13 P82085	P82085 limodyst
27	15	24.6	8	4 Q15894	Q15894 homo sapien
28	15	24.6	8	3 Q34909	Q34909 locusta mig
29	15	24.6	8	13 Q90493	Q90493 eopsaltria
30	15	24.6	9	2 Q43960	Q43960 azotobacter
31	15	24.6	9	4 Q15891	Q15891 homo sapien
32	15	24.6	9	10 Q85306	Q85306 glycine max
33	15	24.6	9	10 Q9FEC0	Q9FEC0 hordeum mori
34	15	24.6	10	5 P82222	P82222 bombyx mori
35	15	24.6	10	10 Q8GZC8	Q8GZC8 hordeum vul
36	15	24.6	10	11 Q61807	Q61807 mus musculu
37	15	24.6	11	3 Q9TR95	Q9TR95 pictia angu
38	15	24.6	11	4 Q9C057	Q9C057 homo sapien
39	15	24.6	11	6 Q9BDC8	Q9BDC8 pongo pygma
40	15	24.6	11	6 Q9BDQ9	Q9BDQ9 gorilla gor
41	15	24.6	11	6 Q9BDD0	Q9BDD0 pan troglod
42	15	24.6	11	6 Q9BDC9	Q9BDC9 pan paniscu
43	15	24.6	12	4 Q9UNV5	Q9UNV5 homo sapien
44	14	23.0	7	8 Q9J182	Q9J182 gnathochobia
45	14	23.0	8	12 Q9J1U9	Q9J1U9 influenza a

## ALIGNMENTS

RESULT 1										
ID	Q9PS71	PRELIMINARY;			PRT;	11 AA.				
AC	Q9PS71									
DT	01-MAY-2000 (TREMBlrel. 13, Created)									
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)									
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)									
DE	Fibrinolytic metalloproteinase (fragment).									
OS	Agkistrodon contortrix									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae;									
OC	Viperidae; Crotalinae; Agkistrodon.									
OX	NCBI_TaxID=8720;									
RN	[1]									
RP	SEQUENCE.									
RX	MEDLINE=91378546; PubMed=1896066;									
RA	Guan A.L., Reizos A.D., Henderson G.N., Markland F.S., Jr.;									
RT	"Purification and characterization of a fibrinolytic enzyme from venom									
RT	of the southern copperhead snake (Agkistrodon contortrix									
RT	contortrix)";									
RL	Arch. Biochem. Biophys. 289:197-207(1991).									
FT	NON TER	11	11							
SQ	SEQUENCE	11 AA;	1209 MW;	7CA02D1D41B8772B CRC64;						
Query Match										
	Best Local Similarity	39.3%;	Score 24;	DB 13;	Length 11;					
	Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
RESULT 2										
ID	Q9TT78	PRELIMINARY;			PRT;	9 AA.				
AC	Q9TT78									
DT	01-MAY-2000 (TREMBlrel. 13, Created)									
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)									



DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Thymidylate synthase (Fragment).  
 GN TS.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21015404; PubMed=11130975;  
 RA Brouillette J.A., Andrew J.R., Venta P.J.;  
 RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence  
 method.";  
 RL Mamm. Genome 11:1079-1086(2000).  
 DR EMBL; AF202073; AAF20918.1; -.  
 FT NON TER 1 1  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 899 MW; 6731A1E059CA867 CRC64;  
  
 QY Query Match 31.1%; Score 19; DB 6; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
 RESULT 3  
 ID 092766 PRELIMINARY; PRT; 9 AA.  
 AC C92766;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE Fusion protein (Fragment).  
 GN F.  
 OS Canine distemper virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.  
 NCBI\_TaxID=11232;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Dog H5526/89;  
 RA Liemann H., Harder T., Haas L.;  
 RT "Genetic analysis of the central untranslated genome region and the  
 proximal coding part of the F gene of wild-type and vaccine distemper  
 morbilliviruses.";  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026237; AAC09167.1; -.  
 FT NON TER 9 9  
 SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;  
  
 QY Query Match 31.1%; Score 19; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 RESULT 4  
 ID 071066 PRELIMINARY; PRT; 9 AA.  
 AC 071066;  
 DT 01-AUG-1998 (TREMBlrel. 07, Created)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Fusion protein (Fragment).  
 GN F.  
 OS Canine distemper virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.  
 NCBI\_TaxID=11232;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Dog #10757/96;  
 RA Liemann H., Harder T., Haas L.;  
 RT "Genetic analysis of the central untranslated genome region and the  
 proximal coding part of the F gene of wild-type and vaccine distemper  
 morbilliviruses.";  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026234; AAC09164.1; -.  
 FT NON TER 9 9  
 SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;  
  
 QY Query Match 31.1%; Score 19; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Db 1 MN 3  
  
 RESULT 5  
 ID P82081 PRELIMINARY; PRT; 12 AA.  
 AC P82081;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 3.  
 OS Limnodynastes terraereginae (Northern banjo frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 NCBI\_TaxID=104894;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=IBIDIAL GLAND;  
 RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 the banjo frogs Limnodynastes terreereginae and Limnodynastes dumerilii and  
 Limnodynastes terraereginae.";  
 RL Aust. J. Chem. 46:833-842(1993).  
 CC -1- MASS SPECTROMETRY: MW=1236; METHOD=FAE.  
 SQ SEQUENCE 12 AA; 1236 MW; 147AA70FDF472724 CRC64;  
  
 QY Query Match 31.1%; Score 19; DB 13; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
 Db 7 LNNIG 11  
  
 RESULT 6  
 ID 013591 PRELIMINARY; PRT; 8 AA.  
 AC 013591;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE ORF YN1337M (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Obermaier B., Piravandi E., Rinke M.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z1612; CAA96271.2; -  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 1005 MW; 5CA441E449C9720 CRC64;  
 Query Match 29.5%; Score 18; DB 3; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 7 FMHN 10  
 DB 4 FMHN 7  
 RESULT 7  
 Q15342 PRELIMINARY; PRT; 10 AA.  
 AC Q15342;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)  
 DE AML1 protein (Fragment).  
 GN AML1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96226397; PubMed=8634147;  
 RA Lavanon D., Bernstein Y., Negreanu V., Ghozi M.C., Bar-Am I.,  
 RA Alevan R., Goldenberg D., Lotem J., Groner Y.;  
 RT "A large variety of alternatively spliced and differentially expressed  
 RT mRNAs are encoded by the human acute myeloid leukemia gene AML1";  
 RL DNA Cell Biol. 15:175-185 (1996).  
 DR EMBL; X90978; CAA62465.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1254 MW; 8D99287B441AF365 CRC64;  
 Query Match 29.5%; Score 18; DB 4; Length 10;  
 Best Local Similarity 44.4%; Pred. No. 8.8e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 SVSEIOFMH 9  
 DB 1 SVSMXRYPH 9  
 RESULT 8  
 Q8M50 PRELIMINARY; PRT; 12 AA.  
 AC Q8M50;  
 DT 01-OCT-2002 (TEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)  
 DE Ribosomal protein 16 (Fragment).  
 GN RPL16.  
 OS Anoda cristata.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Anoda.  
 OX NCBI\_TaxID=193227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Preil B.B., Brubaker C.L., Craven L.A., Crisp M.D.;  
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
 RT chloroplast DNA sequences of ndhF and the rpl16 intron";  
 RL Syst. Bot. 27:333-350 (2002).  
 DR EMBL; AF384867; AA050405.1; -  
 GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.  
 FT NON\_TER 1  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1431 MW; 9A5E5B65452C9CA CRC64;  
 Query Match 29.5%; Score 18; DB 8; Length 12;  
 Best Local Similarity 37.5%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 EIOFMHN 11  
 DB 3 EPDFVNNI 10  
 RESULT 9  
 Q85631 PRELIMINARY; PRT; 12 AA.  
 AC Q85631;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
 DE MH2, proviral DNA, myc to 3' LTR (Fragment).  
 OS Avian carcinoma virus.  
 OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.  
 OX NCBI\_TaxID=11958;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85033920; PubMed=6092695;  
 RA Sutraye P., Jansen H.W., Bister K., Rapp U.R.;  
 RT "3'-terminal region of avian carcinoma virus MH2 shares sequence  
 RT elements with avian sarcoma viruses Y73 and SR-A";  
 RL J. Virol. 52:703-705 (1984).  
 DR EMBL; K03100; AAA44238.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1466 MW; 72E4B884F30736DB CRC64;  
 Query Match 29.5%; Score 18; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 HNL 11  
 DB 2 HNL 4  
 RESULT 10  
 Q23876 PRELIMINARY; PRT; 11 AA.  
 AC Q23876;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)  
 DE Actin 4.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostelidida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82260445; PubMed=6286214;  
 RA McKewen M., Firtel R.A.;  
 RT "Actin multigene family of Dictyostelium";  
 RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505 (1982).  
 DR EMBL; K02957; AAA33150.1; -  
 GO; GO:0009507; C:chloroplast; IEA.  
 Query Match 27.9%; Score 17; DB 5; Length 11;  
 Best Local Similarity 28.6%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 EIOFMHN 10  
 DB 5 DVQALNN 11

## RESULT 11

Q35374 PRELIMINARY; PRT; 11 AA.  
 ID Q35374  
 AC Q35374  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE P1 protein (Fragment).  
 OS Paramacium tetraurelia.  
 OC Microchondrion.  
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Periculida;  
 OC Paramacium.  
 OC NCBI\_TaxID=5688;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=stock 172;  
 RX MEDLINE=87055241; PubMed=3023187;  
 RA Pritchard A.E., Sellmer J.J., Cummings D.J.;  
 RT "Paramacium mitochondrial DNA sequences and RNA transcripts for  
 RT cytochrome oxidase subunit I, URF1, and three ORFs adjacent to the  
 RT replication origin."  
 RL Gene 44:243-253(1986).  
 DR EMBL; M15280; AAA79267.1; -;  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER  
 FT SEQUENCE 11 AA; 1266 MW; 1D84259D16D046D4 CRC64;

Query Match 27.8%; Score 17; DB 8; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQ 6  
 DB 2 SLNQIQ 7

## RESULT 12

Q28742 PRELIMINARY; PRT; 7 AA.  
 ID Q28742  
 AC Q28742  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Alpha-myosin heavy chain (Fragment).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OC NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=84221901; PubMed=6328491;  
 RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,  
 RA Rabinowitz M.;  
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-  
 RT ventricular myosin heavy chains."  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).  
 DR EMBL; K01698; AAA31415.1; -;  
 DR PIR; I46868; I46868.  
 FT NON\_TER  
 FT SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match 26.2%; Score 16; DB 6; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QPMEN 10  
 DB 1 QXMD 5

## RESULT 13

Q8UJ20 PRELIMINARY; PRT; 7 AA.  
 ID Q8UJ20  
 AC Q8UJ20  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Extracellular fatty acid binding protein (Fragment).  
 GN EXFABP.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RA Wang Q., Li N., Li H.;  
 RT "Cloning and sequencing of 3' UTR of EXFABP gene in chicken."  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF487519; AA19665.1; -;  
 FT NON\_TER  
 FT SEQUENCE 7 AA; 780 MW; 72CB1AB2D5BEB370 CRC64;

Query Match 26.2%; Score 16; DB 13; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEI 5  
 DB 3 SVDEV 7

## RESULT 14

Q05403 PRELIMINARY; PRT; 8 AA.  
 ID Q05403  
 AC Q05403  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE DNA for ORF 5 from chromosome XV (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OC NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FY1679;  
 RX MEDLINE=96021609; PubMed=8533473;  
 RA Zimmt E., Pearson B.M., Kalogeropoulos A., Schweizer M.;  
 RT "A 29,425 Kb segment on the left arm of yeast chromosome XV contains  
 RT more than twice as many unknown as known open reading frames."  
 RL Yeast 11:975-986(1995).  
 DR EMBL; X83121; CAA58183.1; -;  
 FT NON\_TER  
 FT SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 26.2%; Score 16; DB 3; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1e+06;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MENTL 11  
 DB 2 INHV 5

## RESULT 15

Q40659 PRELIMINARY; PRT; 8 AA.  
 ID Q40659  
 AC Q40659  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

Tue May 18 12:03:05 2004

us-09-730-174a-4.closed.rspt

Page 5

DE Alpha-amylase (Fragment).  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91078641; PubMed=2258052;  
RA Kumagai M.H., Shan M., Terashima M., Vrkljan Z., Whitaker J.R.,  
RA Rodriguez R.L.;  
RT "Expression and secretion of rice alpha-amylase by saccharomyces  
cerevisiae.";  
RL Gene 94:209-216(1990).  
DR EMBL; M62915; AAA33892.1; -.  
DR Gramene; Q40659; -.  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;

Query Match 26.2%; Score 16; DB 10; Length 8;  
Best Local Similarity 28.6%; Pred. No. 1e+06;  
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 5 IQFMHNL 11  
: : : : :  
Db 1 MOVLINNM 7

Search completed: May 18, 2004, 10:04:47  
Job time : 30.25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:42:39 ; Search time 45.75 Seconds  
(without alignments)  
74.111 Million cell updates/sec

Title: US-09-730-174A-4  
Perfect score: 61  
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	82.0	11	6	ABG72607
2	50	82.0	12	6	ABG72608
3	46	75.4	11	3	AAy96968
4	45	73.8	10	2	AAK1644
5	45	73.8	10	3	AAy68767
6	45	73.8	10	4	AAAB6219
7	45	73.8	10	6	ABR44166
8	41	67.2	9	4	AAAB6225
9	39	63.9	9	2	AAK1645
10	39	63.9	9	3	AAy96981
11	39	63.9	9	4	AAAB6220
12	38.5	59.0	11	2	AAy50600
13	36	59.0	9	3	AAAB1862
14	36	59.0	9	3	AAy96966
15	33	54.1	9	3	AAAB1863
16	33	54.1	10	4	AAAB6932
17	33	54.1	11	4	AAAB6931
18	33	54.1	11	4	AAAB6915
19	33	54.1	11	4	AAAB4770
20	33	54.1	12	4	AAAB6914
21	33	54.1	12	4	AAAB4769
22	32	52.5	9	3	AAy78849
23	31	50.8	8	2	AAAB1646
24	31	50.8	8	3	AAAB7467
25	31	50.8	8	4	AAAB6221

26	31	50.8	10	6	ABP71484	ABP71484 Parathyro
27	31	50.8	11	6	ABP71485	ABP71485 Parathyro
28	31	50.8	11	6	ABP71483	ABP71483 Parathyro
29	31	50.8	12	2	AAW45785	AAW45785 Parathyro
30	31	50.8	12	6	ABP71482	ABP71482 Parathyro
31	29	47.5	9	3	AAAB1866	AAAB1866 Parathyro
32	28	45.9	11	1	AAAB2547	AAAB2547 (asn10, T
33	28	45.9	11	4	AAAB6892	AAAB6892 Rat parat
34	28	45.9	12	4	AAAB6891	AAAB6891 Rat parat
35	27	44.3	10	5	ABG69386	ABG69386 Vascular
36	27	44.3	11	4	ABU54029	ABU54029 Human DNA
37	26	42.6	6	2	AAK1648	AAK1648 Human par
38	26	42.6	6	3	AAy68764	AAy68764 Amino aci
39	26	42.6	6	4	AAAB6223	AAAB6223 Human par
40	26	42.6	6	6	ABR44168	ABR44168 Human par
41	26	42.6	7	2	AAK1647	AAK1647 Human par
42	26	42.6	7	3	AAAB0068	AAAB0068 N-termina
43	26	42.6	7	4	AAAB6222	AAAB6222 Human par
44	26	42.6	9	3	AAAB1864	AAAB1864 PTH(1-14)
45	26	42.6	9	3	AAy97062	AAy97062 PTH-rp N-

ALIGNMENTS

RESULT 1	ABG72607	standard; peptide; 11 AA.
ID	ABG72607	
XX	ABG72607;	
AC	11-FEB-2003	(first entry)
DT	11-FEB-2003	(first entry)
XX	Parathyroid hormone antigenic peptide 2-12.	
DE	Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;	
XX	primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.	
KW	Homo sapiens.	
XX	Mus sp.	
OS	Rattus sp.	
OS	Bos taurus.	
OS	Sus scrofa.	
OS	Canis familiaris.	
XX	Key	Location/Qualifiers
FT	Misc-difference 6	/label= Leu, Phe
FT		
XX	US2002110871-A1.	
PV	15-AUG-2002.	
XX	05-DEC-2000; 2000US-00730174.	
PD	05-DEC-2000; 2000US-00730174.	
XX	05-DEC-2000; 2000US-00730174.	
XX	(ZAHK/) ZAHKADNIX R J.	
PA	(LAVI/) LAVIGNE J R.	
XX	Zahradnik RJ, Lavigne JR,	
PI	WPI; 2003-06685/06.	
XX	New parathyroid hormone (PTH) antigenic peptide inducing the formation	
PT	and isolation of antibodies having an affinity to it; useful for	
PT	mediating bioactive PTH levels in serum, plasma and/or cell culture	
PT	media.	
XX	Claim 1; Page 5; 11p; English.	
XX	The invention relates to a new antigenic peptide for inducing the	
CC	formation and isolation of antibodies having an affinity to it, being	

CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
CC are: (1) a method for producing antibodies useful in the determination of  
CC PTH levels in a biological sample comprising: (a) providing at least one  
CC first peptide antigen comprising a peptide fragment of PTH; (b)  
CC administering the first peptide antigen to a host animal to induce  
CC antibody production; (c) monitoring the antibody titre produced; (d)  
CC isolating antisera produced in the host animal; and (e) selecting  
CC antisera from the isolated antisera produced in the host that is capable  
CC of binding to a second peptide antigen; (2) an antibody (ab) produced by  
CC the method; and (3) test kits and analytical procedures used for the  
CC determination of bioactive intact PTH utilising (ab). The methods and  
CC compositions of the present invention are useful for determining  
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
CC The antigens, antibodies and methods of the present invention, as  
CC compared to prior art, have the particular advantages of possessing  
CC greater affinity for PTH, and in particular, are designed to have a novel  
CC recognition for amino acid residues extending beyond the first N-terminal  
CC PTH residue, and further have negligible cross-reactivity with the large  
CC non-molecular forms of PTH. PTH levels are an important parameter in  
CC patients suffering from hypercalcaemia, osteoporosis and primary  
CC hyperparathyroidism. The present sequence represents a PTH antigenic  
CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,  
CC canine and bovine PTH  
CC  
XX  
SQ Sequence 11 AA;

Query Match 82.0%; Score 50; DB 6; Length 11;  
Best Local Similarity 90.9%; Pred. No. 0.01;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 VSEIQFMNIG 12  
DB 1 VSEIQXMHNLG 11

RESULT 2  
ABG72608  
ID ABG72608 standard; peptide; 12 AA.  
XX  
AC ABG72608;  
XX  
DT 11-FEB-2003 (first entry)  
XX  
DE Parathyroid hormone antigenic peptide 1-12.  
XX  
XX Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;  
KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.  
XX  
XX Homo sapiens.  
OS Mus sp.  
OS Rattus sp.  
OS Bos taurus.  
OS Sus scrofa.  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /label= Ser, Ala  
FT Misc-difference 7 /label= Leu, Phe  
FT  
XX  
XX US2002110871-A1.  
XX  
XX 15-AUG-2002.  
XX  
XX 05-DEC-2000; 2000US-00730174.  
XX  
XX 05-DEC-2000; 2000US-00730174.  
XX  
XX (ZAHAR/) ZAHARADNIK R J.  
XX (LAVI/) LAVIGNE J R.  
XX  
XX Zahradnik RJ, Lavigne JR;  
PI

XX  
DR MPI; 2003-066685/06.  
XX  
XX New parathyroid hormone (PTH) antigenic peptide inducing the formation  
PT and isolation of antibodies having an affinity to it, useful for  
PT determining bioactive PTH levels in serum, plasma and/or cell culture  
PT media.  
XX  
PS Claim 2; Page 5; 11pp; English.

XX The invention relates to a new antigenic peptide for inducing the  
XX formation and isolation of antibodies having an affinity to it, being  
CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
CC are: (1) a method for producing antibodies useful in the determination of  
CC PTH levels in a biological sample comprising: (a) providing at least one  
CC first peptide antigen comprising a peptide fragment of PTH; (b)  
CC administering the first peptide antigen to a host animal to induce  
CC antibody production; (c) monitoring the antibody titre produced; (d)  
CC isolating antisera produced in the host animal; and (e) selecting  
CC antisera from the isolated antisera produced in the host that is capable  
CC of binding to a second peptide antigen; (2) an antibody (ab) produced by  
CC the method; and (3) test kits and analytical procedures used for the  
CC determination of bioactive intact PTH utilising (ab). The methods and  
CC compositions of the present invention are useful for determining  
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
CC The antigens, antibodies and methods of the present invention, as  
CC compared to prior art, have the particular advantages of possessing  
CC greater affinity for PTH, and in particular, are designed to have a novel  
CC recognition for amino acid residues extending beyond the first N-terminal  
CC PTH residue, and further have negligible cross-reactivity with the large  
CC non-molecular forms of PTH. PTH levels are an important parameter in  
CC patients suffering from hypercalcaemia, osteoporosis and primary  
CC hyperparathyroidism. The present sequence represents a PTH antigenic  
CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,  
CC canine and bovine PTH  
CC  
XX  
SQ Sequence 12 AA;

Query Match 82.0%; Score 50; DB 6; Length 12;  
Best Local Similarity 90.9%; Pred. No. 0.011;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 VSEIQFMNIG 12  
DB 2 VSEIQXMHNLG 12

RESULT 3  
AA96968  
ID AA96968 standard; peptide; 11 AA.  
XX  
AC AA96968;  
XX  
DT 31-OCT-2000 (first entry)  
XX  
DE Parathyroid hormone N-terminal signaling domain (residues 1-11).  
XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
KW bone reformation; resorption; remodeling; tether; osteoporosis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2000039278-A2.  
XX  
XX 06-JUL-2000.  
XX  
XX 30-DEC-1999; 99WO-US031106.  
XX  
XX 31-DEC-1998; 98US-0114577P.  
XX  
XX (GARD/) GARDELLA T J.  
XX (KRON/) KRONENBERG H M.  
XX (POTT/) POTTS J T.  
PA

(JUEP/) JUEPNER H.

Gardella TV, Kronenberg HW, Potts JT, Juepner H;  
WPI; 2000-452384/39.

New compound comprising an amino terminal signaling functional domain  
linked to a carboxy-terminal binding portion of parathyroid hormone for  
treating mammalian conditions characterized by decreases in bone mass.

Claim 4; Page 92; 119pp; English.

Compounds of the structure or formula S-(L)<sub>n</sub>-B, R<sub>1</sub>-S-(L)<sub>n</sub>-R or S-(L)<sub>n</sub>-  
R, are new. S is an amino terminal signaling functional domain of  
parathyroid hormone (PTH); L is a linker molecule present n times (where  
n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R<sub>1</sub> is the  
PTH-1 receptor signal sequence; and R is a portion of PTH-1 receptor  
sequence. The new compounds are used for treating mammalian conditions  
characterized by decreases in bone mass, determining rates of bone  
reformation, bone resorption and/or bone remodeling, treating diseases  
and disorders associated with decreased telhetyl activity, increasing CAMP  
in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
non-peptide PTH (claimed). The new compound can be administered by  
inhalation unlike the large native PTH or PTHrp which avoids the need for  
regular injections to treat osteoporosis

Sequence 11 AA;

Query Match 75.4%; Score 46; DB 3; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.059;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMHNL 11

DB 1 AVSEIQLMHNL 11

RESULT 4

AAR91644

ID AAR91644 standard; peptide; 10 AA.

AAR91644;

06-NOV-1996 (first entry)

Human parathyroid hormone antigenic peptide hPTH 1-10.

Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
diagnosis; active hPTH 1-37.

Synthetic.

DE4434551-A1.

04-APR-1996.

28-SEP-1994; 94DE-04434551.

28-SEP-1994; 94DE-04434551.

(FORS/) FORSSMANN W.

Adermann K, Forssmann W, Hock D, Maegerlein M;

WPI; 1996-180391/19.

New antigenic peptide(s) from human parathyroid hormone - and antibodies  
generated using them, able to distinguish between active and inactive  
forms of the hormone.

Claim 2; Page 4; 5pp; German.

The present sequence is a specific example of claimed immunogenic  
peptides having a sequence from hPTH(1-37) which includes the N- or C-  
terminal alpha-helical region and/or the non-structured region of the  
hormone. Antibodies and their binding fragments generated by injecting an  
animal with the peptides are useful as diagnostic reagents for  
determination of biologically active hPTH(1-37)

Sequence 10 AA;

Query Match 73.8%; Score 45; DB 2; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.082;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMHNL 10

DB 1 SVSEIQLMHNL 10

RESULT 5

AAV68767

ID AAV68767 standard; peptide; 10 AA.

AAV68767;

05-MAY-2000 (first entry)

Amino acids 1-10 of a parathyroid hormone (PTH).

Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;  
slimming treatment; cellulite; skin firming.

Undenified.

WO200004047-A1.

27-JAN-2000.

07-JUL-1999; 99WO-FR001687.

17-JUL-1998; 98FR-00009193.

(SEDE-) SEDERMA.

Lantner K;

WPI; 2000-171243/15.

New parathyroid hormone fragment peptides, used as lipolysis stimulants  
in topically applied cosmetic compositions for slimming treatment of  
excessive weight in hips and thighs.

Claim 1; Page 8; 18pp; French.

The present sequence represents a parathyroid hormone (PTH) fragment,  
comprising amino acids 1-10. Parathyroid hormone fragments of the  
invention have lipolysis stimulating activity (especially when topically  
administered). The lipolytic activity of the peptides is enhanced when  
they are chemically modified to increase their lipophilicity. The  
peptides are used in cosmetic or dermatological compositions for skin  
care. They are especially used for slimming treatment of excessive weight  
in the thighs and hips, in the treatment of cellulite and for skin  
firming

Sequence 10 AA;

Query Match 73.8%; Score 45; DB 3; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.082;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMHNL 10

DB 1 SVSEIQLMHNL 10

RESULT 6  
AAB86219  
ID AAB86219 standard; peptide; 10 AA.  
XX  
XX AAB86219;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
XX Human parathyroid hormone immunogenic peptide SEQ ID 1.  
XX  
XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
KM diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
KM hypo-parathyroidism; hyper-parathyroidism.  
XX  
XX Homo sapiens.  
OS  
XX DE19961350-A1.  
XX  
XX 21-JUN-2001.  
XX  
XX 17-DEC-1999; 99DE-01061350.  
XX  
XX 17-DEC-1999; 99DE-01061350.  
XX  
XX (IMMU-) IMMUNODIAGNOSTIK AG.  
XX  
XX Armbruster FP;  
XX  
XX WPI; 2001-376318/40.  
XX  
XX Determining the content of physiologically active parathyroid hormone,  
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
PT reactive with different epitopes.  
XX  
XX  
XX Disclosure; Page 3; 10pp; German.  
XX  
XX This invention describes a novel method for determining (M1) the content  
CC of active parathyroid hormone (A) by treating a sample with (i) antibody  
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
CC and including the N-terminal residue and (ii) antibody (Ab2) that  
CC recognizes an epitope within the receptor-binding site of (A). The number  
CC of molecules that react with both antibodies is determined and used to  
CC calculate the content of physiologically active (A). The method is used  
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
CC active and (ii) that apparently intact peptide may be biologically  
CC inactive, and also takes into account the fact that some fragments of (A)  
CC are antagonistic (these have the receptor-binding site but lack the N-  
CC terminus). It thus provides a true measure of the content of  
CC physiologically active (A); contrast methods that measure intact peptide  
CC and its 1-37 fragment which may produce falsely high values. This  
CC sequence represents a peptide fragment used to illustrate the method of  
CC the invention  
XX  
XX  
XX Sequence 10 AA;  
SQ  
Query March 73.8%; Score 45; DB 4; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.082;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DT 04-AUG-2003 (first entry)  
XX  
XX Human parathyroid hormone (hPTH) fragment (residues 1-10).  
DE  
XX  
XX Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;  
KM lipolysis; human; hPTH.  
XX  
XX Homo sapiens.  
OS  
XX WO2003035697-A1.  
XX  
XX 01-MAY-2003.  
XX  
XX 06-MAY-2002; 2002WO-KR000835.  
XX  
XX 27-SEP-2001; 2001KR-00060245.  
XX  
XX 15-MAR-2002; 2002KR-00014062.  
XX  
XX (GLDS ) LG HOUSEHOLD & HEALTH CARE LTD.  
XX  
XX Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H;  
XX Chang M;  
XX  
XX WPI; 2003-468288/44.  
XX  
XX Novel fusion peptide comprising self cell-penetrating Tat peptide bound  
PT to human parathyroid hormone-derived peptide, useful as component of skin  
PT slimming cosmetic composition.  
XX  
XX Claim 5; Page 6; 32pp; English.  
XX  
XX The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-  
CC penetrating Tat peptide is bound to human parathyroid hormone-derived  
CC peptide (hPTHDP). The fusion peptide is useful as a component of skin  
CC slimming cosmetic composition. The fusion peptide does not cause  
CC irritation, easily and safely penetrates into integument and endothelium,  
CC does not cause skin disease and has superior lipolysis effects, and is  
CC durable. The present sequence represents a human parathyroid hormone  
CC (hPTH) fragment that can be used to construct the fusion peptide  
XX  
XX  
XX Sequence 10 AA;  
SQ  
Query March 73.8%; Score 45; DB 6; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.082;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMHN 10  
DB 1 SVSEIQFMHN 10

RESULT 8  
AAB86225  
ID AAB86225 standard; peptide; 9 AA.  
XX  
XX AAB86225;  
XX  
XX 03-SEP-2001 (first entry)  
XX  
XX Human parathyroid hormone immunogenic peptide SEQ ID 7.  
DE  
XX  
XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
KM diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
KM hypo-parathyroidism; hyper-parathyroidism.  
XX  
XX Homo sapiens.  
OS  
XX DE19961350-A1.  
XX  
XX 21-JUN-2001.  
XX  
XX 17-DEC-1999; 99DE-01061350.  
XX



PR 17-DEC-1999; 99DE-01061350.  
 XX (IMMU-) IMMUNDIAGNOSTIK AG.  
 XX  
 XX Armbruster FP;  
 XX  
 DR WPI; 2001-376318/40.  
 XX  
 XX Determining the content of physiologically active parathyroid hormone,  
 PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
 PT reactive with different epitopes.  
 XX  
 PS Disclosure; Page 3; 10pp; German.  
 XX  
 CC This invention describes a novel method for determining (M1) the content  
 CC of active parathyroid hormone (A) by treating a sample with (i) antibody  
 CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
 CC and including the N-terminal residue and (ii) antibody (Ab2) that  
 CC recognizes an epitope within the receptor-binding site of (A). The number  
 CC of molecules that react with both antibodies is determined and used to  
 CC calculate the content of physiologically active (A). The method is used  
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
 CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
 CC active and (ii) that apparently intact peptide may be biologically  
 CC inactive, and also takes into account the fact that some fragments of (A)  
 CC are antagonistic (these have the receptor-binding site but lack the N-  
 CC terminus). It thus provides a true measure of the content of  
 CC physiologically active (A); contrast methods that measure intact peptide  
 CC and its 1-37 fragment which may produce falsely high values. This  
 CC sequence represents a peptide fragment used to illustrate the method of  
 CC the invention  
 XX  
 SQ Sequence 9 AA;  
 Query Match 67.2%; Score 41; DB 4; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VSEIQFMEN 10  
 Db 1 VSEIQFMEN 9  
 RESULT 9  
 AAR91645  
 ID AAR91645 standard; peptide; 9 AA.  
 XX  
 AC AAR91645;  
 XX  
 DT 06-NOV-1996 (first entry)  
 XX  
 DE Human parathyroid hormone antigenic peptide hPTH 1-9.  
 XX  
 KM Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
 KM diagnosis; active hPTH 1-37.  
 XX  
 OS Synthetic.  
 XX  
 PN DE434551-A1.  
 XX  
 PD 04-APR-1996.  
 XX  
 PF 28-SEP-1994; 94DE-04434551.  
 XX  
 PR 28-SEP-1994; 94DE-04434551.  
 XX  
 PA (FORS/) FORSSMANN W.  
 XX  
 PI Adgermann K, Forssmann W, Hock D, Maegerlein M;  
 XX  
 DR WPI; 1996-180391/19.  
 XX

PT New antigenic peptide(s) from human parathyroid hormone - and antibodies  
 PT generated using them, able to distinguish between active and inactive  
 PT forms of the hormone.  
 XX  
 XX Claim 2; Page 4; 5pp; German.  
 XX  
 CC The present sequence is a specific example of claimed immunogenic  
 CC peptides having a sequence from hPTH(1-37) which includes the N- or C-  
 CC terminal alpha-helical region and/or the non-structured region of the  
 CC hormone. Antibodies and their binding fragments generated by injecting an  
 CC animal with the peptides are useful as diagnostic reagents for  
 CC determination of biologically active hPTH(1-37)  
 CC  
 SQ Sequence 9 AA;  
 Query Match 63.9%; Score 39; DB 2; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SVSEIQFMH 9  
 Db 1 SVSEIQFMH 9  
 RESULT 10  
 AAY96981  
 ID AAY96981 standard; peptide; 9 AA.  
 XX  
 AC AAY96981;  
 XX  
 DT 31-OCT-2000 (first entry)  
 XX  
 DE Parathyroid hormone N-terminal signaling domain.  
 XX  
 KM PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
 KM bone reformation; resorption; remodeling; tetracycline; osteoporosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200039278-A2.  
 XX  
 PD 06-JUL-2000.  
 XX  
 PF 30-DEC-1999; 99WO-US031108.  
 XX  
 PR 31-DEC-1998; 98US-0114577P.  
 XX  
 PA (GARD/) GARDELLA T J.  
 PA (KRON/) KRONENBERG H M.  
 PA (POTT/) POTTS J T.  
 PA (JUEP/) JUEPNER H.  
 XX  
 PI Gardella TJ, Kronenberg HM, Potts JT, Juepner H;  
 XX  
 DR WPI; 2000-452384/39.  
 XX  
 PT New compound comprising an amino terminal signaling functional domain  
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
 PT treating mammalian conditions characterized by decreases in bone mass.  
 XX  
 PS Claim 11; Page 93; 119pp; English.  
 XX  
 CC Compounds of the structure or formula S-(L)-n-B, R1-S-(L)-n-R or S-(L)-n  
 CC -R, are new. S is an amino terminal signaling functional domain of  
 CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
 CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
 CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the  
 CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
 CC sequence. The new compounds are used for treating mammalian conditions  
 CC characterized by decreases in bone mass, determining rates of bone  
 CC reformation, bone resorption and/or bone remodeling, treating diseases  
 CC and disorders associated with decreased bone activity, increasing BMP  
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or

CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHp which avoids the need for  
CC regular injections to treat osteoporosis  
XX  
SQ Sequence 9 AA;

Query Match 63.9%; Score 39; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIOFMH 9  
1 SVSEIOFMH 9  
DB 1 SVSEIOFMH 9

RESULT 11  
AAB86220 standard; peptide; 9 AA.

AC AAB86220;  
XX  
DT 03-SEP-2001 (first entry)

DE Human parathyroid hormone immunogenic peptide SEQ ID 2.

XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
KW hypo-parathyroidism; hyper-parathyroidism.

XX Homo sapiens.

XX DE19961350-A1.

XX PD 21-JUN-2001.

XX PF 17-DEC-1999; 99DE-01061350.

XX PR 17-DEC-1999; 99DE-01061350.

XX PA (IMMU-) IMMUNDIAGNOSTIK AG.

XX Armbruster FP;

XX WPI; 2001-376318/40.

XX Determining the content of physiologically active parathyroid hormone,  
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
PT reactive with different epitopes.

XX Disclosure; Page 3; 10pp; German.

XX This invention describes a novel method for determining (M1) the content  
CC of active parathyroid hormone (A) by treating a sample with (i) antibody  
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
CC and including the N-terminal residue and (ii) antibody (Ab2) that  
CC recognizes an epitope within the receptor-binding site of (A). The number  
CC of molecules that react with both antibodies is determined and used to  
CC calculate the content of physiologically active (A). The method is used  
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
CC active and (ii) that apparently intact peptide may be biologically  
CC inactive, and also takes into account the fact that some fragments of (A)  
CC are antagonistic (these have the receptor-binding site but lack the N-  
CC terminus). It thus provides a true measure of the content of  
CC physiologically active (A); contrast methods that measure intact peptide  
CC and its 1-37 fragment which may produce falsely high values. This  
CC sequence represents a peptide fragment used to illustrate the method of  
CC the invention

XX Sequence 9 AA;

Query Match 63.9%; Score 39; DB 4; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIOFMH 9  
1 SVSEIOFMH 9  
DB 1 SVSEIOFMH 9

RESULT 12  
AAV50600 standard; peptide; 11 AA.

AC AAV50600;  
XX  
DT 09-FEB-2000 (first entry)

DE Resin bound cyclic peptide 33.

XX Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;  
KW hypotensive; PTH receptor; treatment; hyper-calcaemia; hypo-calcaemia;  
KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;  
KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "FMOC-Ala"

FT Misc-difference 3 /note= "Ser(OctBu)"

FT Misc-difference 4 /note= "Glu(OctBu)"

FT Misc-difference 6 /note= "Gln(Trt)"

FT Misc-difference 9 /note= "His(Trt)"

FT Misc-difference 10 /note= "Asn(Trt)"

XX WO952933-A1.

XX PD 21-OCT-1999.

XX PF 15-APR-1999; 99WO-US008435.

XX PR 15-APR-1998; 96US-0081897P.

XX PA (RHON) RHONE-POULENC RORER PHARM INC.

XX Siedeski AW, Mancel JF;

XX WPI; 1999-633822/54.

XX Convergent synthesis of peptides for treating e.g. bone disorders.

XX Disclosure; Page 75; 85pp; English.

XX This invention describes a novel method for the preparation of peptides  
CC (II) that contain both cyclic and linear peptide fragments comprises  
CC sequential reaction of a resin-bound linear fragment with the cyclic  
CC fragment in N-protected form and optionally other linear fragments. The  
CC products of the invention have osteopathic and hypotensive activity. (II)  
CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The  
CC method is particularly used to prepare cyclic peptide analogs or  
CC parathyroid hormone (PTH) or PTH-related peptides which are useful for  
CC treating diseases that respond to treatment with agents that bind to PTH  
CC receptors (with or without activation of adenyl cyclase activity), e.g.  
CC hyper- or hypo-calcaemia, osteoporosis, osteopenia, hyper- or hypo-  
CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also  
CC for promoting repair of bone fractures. Separate synthesis of the cyclic  
CC fragment allows convergent synthesis of resin-bound (II), with better  
CC yields and higher throughput. The difficulties associated with  
CC preparation of the bridged fragment are confined to a small peptide which

CC can be purified before reaction with the resin-bound component. AAY50568-  
CC Y50614 represent the peptide fragments described in the method of the  
CC invention  
XX  
SQ Sequence 11 AA:  
Query Match 63.1%; Score 38.5; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.5;  
Matches 9; Conservative 2; Mismatches 0; Indels 1; Gaps 1;  
1 SVSEIQFMNLG 12  
1 AVSEIQ-LNLHG 11  
Db  
RESULT 13  
AAB01862  
ID AAB01862 standard; peptide; 9 AA.  
XX  
AC AAB01862;  
XX  
DT 11-SEP-2000 (first entry)  
XX  
XX PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.  
XX  
KM Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;  
KM calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;  
KM bone synthesis; agonist; osteoporosis; non-parenteral delivery.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200023594-A1.  
XX  
PD 27-APR-2000.  
XX  
PF 20-OCT-1999; 99WO-US024481.  
XX  
PR 22-OCT-1998; 98US-0105530P.  
XX  
XX (GARD/) GARDELLA T J.  
PA (KRON/) KRONENBERG H M.  
PA (POTT/) POTTS J T.  
PA (JUEP/) JUEPPNER H.  
XX  
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX  
XX WPI; 2000-339693/29.  
XX  
XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
XX acids that encode them, useful for treating osteoporosis.  
XX  
XX Disclosure; Page 26; 73pp; English.  
XX  
XX The invention relates to a novel parathyroid hormone (PTH) peptide  
XX (AAB01862) and parathyroid hormone-related peptide (PTHrP, AAB01861), and  
XX biologically active derivatives thereof (AAB01867-B01868, AAB01861-  
XX B01869). The peptides of the invention are at least 85% identical to the  
XX generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-  
XX Gly-Lys-X6 (AAB01867) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
XX Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
XX provided that the peptide is not PTHrP(1-14). The peptides of the  
XX invention also encompass fragments of peptides of the invention  
XX consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
XX terminal derivatives. PTH is a major regulator of calcium homeostasis,  
XX and is necessary for the normal function of the gastrointestinal,  
XX skeletal, neurological system, neuromuscular and cardiovascular systems.  
XX It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
XX and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
XX effect on the skeleton, and mediates calcium reabsorption, enhances  
XX phosphate clearance and vitamin D synthesis in the kidney. A homologous  
XX calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
XX the renal and skeletal actions of PTH, and also bind to the PTH-1

CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
CC conditions characterized by a decrease in bone mass, such as  
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
CC medical disorders that arise from excessive or altered action of the PTH-  
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
CC useful in the determination of rates of bone formation, bone resorption  
CC and/or bone remodeling in a patient. The peptides of the invention are  
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
CC conventional synthetic chemistry, and can be delivered to a patient via  
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
CC PTH-1/PTH-2 receptor agonists  
XX  
SQ Sequence 9 AA:  
Query Match 59.0%; Score 36; DB 3; Length 9;  
Best Local Similarity 77.8%; Pred. No. 1.4e+06;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
1 SVSEIQFMH 9  
1 AVSEIQQLMH 9  
Db  
RESULT 14  
AAY96966  
ID AAY96966 standard; peptide; 9 AA.  
XX  
AC AAY96966;  
XX  
DT 31-OCT-2000 (first entry)  
XX  
XX Parathyroid hormone N-terminal signaling domain (residues 1-9).  
XX  
XX PTH, parathyroid hormone, N-terminal; signaling domain; bone mass;  
XX bone reformation; resorption; remodeling; tether; osteoporosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200039278-A2.  
XX  
PD 06-JUL-2000.  
XX  
PF 30-DEC-1999; 99WO-US031108.  
XX  
PR 31-DEC-1998; 98US-0114577P.  
XX  
XX (GARD/) GARDELLA T J.  
PA (KRON/) KRONENBERG H M.  
PA (POTT/) POTTS J T.  
PA (JUEP/) JUEPPNER H.  
XX  
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX  
XX WPI; 2000-452384/39.  
XX  
XX New compound comprising an amino terminal signaling functional domain  
XX linked to a carboxy-terminal binding portion of parathyroid hormone for  
XX treating mammalian conditions characterized by decreases in bone mass.  
XX  
XX Claim 4; Page 92; 119pp; English.  
XX  
XX Compounds of the structure or formula S (L)<sub>n</sub>-B, R1-S-(L)<sub>n</sub>-R or S-(L)<sub>n</sub>-  
XX -R, are new. S is an amino terminal signaling functional domain of  
XX parathyroid hormone (PTH); L is a linker molecule present n times (where  
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the  
XX PTH-1 receptor signal sequence; and R is a portion of PTH-1 receptor  
XX sequence. The new compounds are used for treating mammalian conditions  
XX characterized by decreases in bone mass, determining rates of bone  
XX reformation, bone resorption and/or bone remodeling, treating diseases

CC and disorders associated with decreased lethral activity, increasing cAMP  
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
 CC regular injections to treat osteoporosis

XX Sequence 9 AA;

Query Match 59.0%; Score 36; DB 3; Length 9;  
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMH 9  
 :|||||:  
 Db 1 AVSEIQQLMH 9

RESULT 15

ID AAB01863 standard; peptide: 9 AA.

XX AAB01863;

DT 11-SEP-2000 (first entry)

DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.

XX Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;  
 KW calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;  
 XX bone synthesis; agonist; osteoporosis; non-parenteral delivery.

OS Homo sapiens.  
 XX Synthetic.

XX MO200023594-A1.

PD 27-APR-2000.

XX 20-OCT-1999; 99WO-US024481.

XX 22-OCT-1998; 98US-0105530P.

PA (GARD/) GARDELLA T J.

PA (KRON/) KRONENBERG H M.

PA (POTS/) POTTS J T.

PA (JUEP/) JUEPNER H.

PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

DR WPI, 2000-339693/29.

PT Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
 PT acids that encode them, useful for treating osteoporosis.

XX Disclosure: Page 26; 73pp; English.

XX The invention relates to a novel parathyroid hormone (PTH) peptide  
 CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and  
 CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
 CC B01869). The peptides of the invention are at least 85% identical to the  
 CC generic peptide of the formula: X1-Ser or Ala; X2-Ile or Lys; X3-Ile  
 CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
 CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;

CC provided that the peptide is not PTHrP(1-14). The peptides of the  
 CC invention also encompass fragments of peptides of the invention  
 CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
 CC terminal derivatives. PTH is a major regulator of calcium homeostasis,  
 CC and is necessary for the normal function of the gastrointestinal,  
 CC skeletal, neurological system, neuromuscular and cardiovascular systems.

CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
 CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
 CC effect on the skeleton, and mediates calcium reabsorption, enhances  
 CC phosphate clearance and vitamin D synthesis in the kidney. A homologous

CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
 CC the renal and skeletal actions of PTH, and also bind to the PTH-1  
 CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
 CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
 CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
 CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
 CC conditions characterized by a decrease in bone mass, such as  
 CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
 CC medical disorders that arise from excessive or altered action of the PTH-  
 CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
 CC useful in the determination of rates of bone formation, bone resorption  
 CC and/or bone remodelling in a patient. The peptides of the invention are  
 CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
 CC conventional synthetic chemistry, and can be delivered to a patient via  
 CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
 CC PTH-1/PTH-2 receptor agonists

XX Sequence 9 AA;

Query Match 54.1%; Score 33; DB 3; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMH 9  
 :|||||:  
 Db 1 AVSEIQQLMH 9

Search completed: May 18, 2004, 10:01:54  
 Job time : 46.75 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 10:04:51 ; Search time 33.25 Seconds  
(without alignments)  
100.425 Million cell updates/sec

Title: US-09-730-174A-4  
Perfect score: 61  
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 166097

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCF\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCFS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US10G\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	61	100.0	12 9 US-09-730-174A-4	Sequence 4, Appli
2	58	95.1	12 9 US-09-730-174A-6	Sequence 6, Appli
3	57	93.4	11 9 US-09-730-174A-2	Sequence 2, Appli
4	55	90.2	12 9 US-09-730-174A-3	Sequence 3, Appli
5	52	85.6	12 9 US-09-730-174A-5	Sequence 5, Appli
6	51	83.2	11 9 US-09-730-174A-1	Sequence 1, Appli
7	45	73.8	10 14 US-10-168-185-1	Sequence 7, Appli
8	41	67.2	9 14 US-10-168-185-7	Sequence 2, Appli
9	39	63.9	8 14 US-10-168-185-2	Sequence 8, Appli
10	37	60.7	8 14 US-10-168-185-8	Sequence 6, Appli
11	36	59.0	9 14 US-10-192-673-6	Sequence 6, Appli
12	35	54.1	9 14 US-10-192-673-7	Sequence 7, Appli
13	31	50.8	8 14 US-10-168-185-3	Sequence 3, Appli
14	29	47.5	9 14 US-10-192-673-10	Sequence 10, Appli
15	27	44.3	10 14 US-10-033-741-61	Sequence 61, Appli

16	26	42.6	6 14 US-10-168-185-5	Sequence 5, Appli
17	26	42.6	7 14 US-10-168-185-4	Sequence 4, Appli
18	26	42.6	7 14 US-10-192-673-8	Sequence 8, Appli
19	26	42.6	10 15 US-10-168-185-11	Sequence 11, Appli
20	25	41.0	10 15 US-10-137-867-526	Sequence 2, Appli
21	25	41.0	10 15 US-10-366-709-2	Sequence 45, Appli
22	24	39.3	9 9 US-09-834-765-45	Sequence 55, Appli
23	24	39.3	9 9 US-09-834-765-55	Sequence 6, Appli
24	24	39.3	9 9 US-09-746-945-6	Sequence 73, Appli
25	24	39.3	10 9 US-09-834-765-73	Sequence 78, Appli
26	24	39.3	10 9 US-09-834-765-78	Sequence 8, Appli
27	24	39.3	10 14 US-10-233-187-8	Sequence 14, Appli
28	24	39.3	11 14 US-10-153-334-14	Sequence 16, Appli
29	24	39.3	12 14 US-10-319-130-16	Sequence 508, Appli
30	23	37.7	8 14 US-10-043-487-508	Sequence 26, Appli
31	23	37.7	9 14 US-10-147-140-26	Sequence 120, Appli
32	23	37.7	9 15 US-10-024-652-120	Sequence 339, Appli
33	23	37.7	9 15 US-10-024-652-339	Sequence 407, Appli
34	23	37.7	9 15 US-10-024-652-407	Sequence 956, Appli
35	23	37.7	9 15 US-10-024-652-956	Sequence 1094, Appli
36	23	37.7	9 15 US-10-024-652-1094	Sequence 1259, Appli
37	23	37.7	9 15 US-10-024-652-1259	Sequence 1464, Appli
38	23	37.7	9 15 US-10-024-652-1464	Sequence 2057, Appli
39	23	37.7	9 15 US-10-024-652-2057	Sequence 2058, Appli
40	23	37.7	9 15 US-10-024-652-2058	Sequence 4, Appli
41	23	37.7	10 9 US-09-976-787-4	Sequence 12, Appli
42	23	37.7	10 9 US-09-865-198-4	Sequence 41, Appli
43	23	37.7	10 9 US-09-865-099-12	
44	23	37.7	10 9 US-09-563-222-41	
45	23	37.7	10 10 US-09-563-222-41	

## ALIGNMENTS

RESULT 1  
US-09-730-174A-4  
Sequence 4, Application US/09730174A  
Patent No. US20020110871A1  
GENERAL INFORMATION:  
APPLICANT: Zahradnik, R.J.  
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Hc  
FILE REFERENCE: IMUNE-001A  
CURRENT APPLICATION NUMBER: US/09/730,174A  
CURRENT FILING DATE: 2000-12-05  
NUMBER OF SEQ ID NOS: 12  
SEQ ID NO 4  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
US-09-730-174A-4

Query Match 100.0% Score 61, DB 9, Length 12;  
Best Local Similarity 100.0% Pred No. 0/100013;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQFMHNLG 12  
DB 1 SVSEIQFMHNLG 12

RESULT 2  
US-09-730-174A-6  
Sequence 6, Application US/09730174A  
Patent No. US20020110871A1  
GENERAL INFORMATION:  
APPLICANT: Zahradnik, R.J.  
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Hc  
FILE REFERENCE: IMUNE-001A

Tue May 18 12:03:04 2004

us-09-730-174a-4.closed.rapb

Page 2

```

; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-6
```

```

Query Match      95.1%; Score 58; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.00047;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 VSEIQFMHNLG 12
Db      1 AVSEIQFMHNLG 12
```

```

RESULT 3
US-09-730-174A-2
; Sequence 2, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-2
```

```

Query Match      93.4%; Score 57; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 VSEIQFMHNLG 12
Db      1 VSEIQFMHNLG 11
```

```

RESULT 4
US-09-730-174A-3
; Sequence 3, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3
```

```

Query Match      90.2%; Score 55; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 VSEIQFMHNLG 12
Db      1 VSEIQFMHNLG 12
```

```

RESULT 5
US-09-730-174A-5
; Sequence 5, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5
```

```

Query Match      85.2%; Score 52; DB 9; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.0061;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 VSEIQFMHNLG 12
Db      1 AVSEIQFMHNLG 12
```

```

RESULT 6
US-09-730-174A-1
; Sequence 1, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1
```

```

Query Match      83.6%; Score 51; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0085;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 VSEIQFMHNLG 12
Db      1 VSEIQFMHNLG 11
```

```

RESULT 7
US-10-168-185-1
; Sequence 1, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
```

;; TITLE OF INVENTION: Activity in a Human Sample  
;; FILE REFERENCE: HLZ-004US  
;; CURRENT APPLICATION NUMBER: US/10/168,185  
;; PRIOR FILING DATE: 2002-06-17  
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911  
;; PRIOR FILING DATE: 2000-12-18  
;; PRIOR APPLICATION NUMBER: DE 19961350  
;; PRIOR FILING DATE: 1999-12-17  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-168-185-1

Query Match 73.8%; Score 45; DB 14; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.098;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQPMHN 10  
Db 1 SVSEIQPMHN 10

RESULT 8  
US-10-168-185-7  
;; Sequence 7, Application US/10168185  
;; Publication No. US20030175802A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Armbruster, Franz Paul  
;; APPLICANT: Missbichler, Albert  
;; APPLICANT: Schmidt-Gayk, Heinrich  
;; APPLICANT: Roth, Heinz-Jürgen  
;; TITLE OF INVENTION: Method for Determining Parathormone  
;; FILE REFERENCE: HLZ-004US  
;; CURRENT APPLICATION NUMBER: US/10/168,185  
;; PRIOR FILING DATE: 2002-06-17  
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911  
;; PRIOR FILING DATE: 2000-12-18  
;; PRIOR APPLICATION NUMBER: DE 19961350  
;; PRIOR FILING DATE: 1999-12-17  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 7  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-168-185-7

Query Match 67.2%; Score 41; DB 14; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1e+06;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQPMHN 10  
Db 1 VSEIQPMHN 9

RESULT 9  
US-10-168-185-2  
;; Sequence 2, Application US/10168185  
;; Publication No. US20030175802A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Armbruster, Franz Paul  
;; APPLICANT: Missbichler, Albert  
;; APPLICANT: Schmidt-Gayk, Heinrich  
;; APPLICANT: Roth, Heinz-Jürgen  
;; TITLE OF INVENTION: Method for Determining Parathormone  
;; FILE REFERENCE: HLZ-004US  
;; CURRENT APPLICATION NUMBER: US/10/168,185

;; CURRENT FILING DATE: 2002-06-17  
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911  
;; PRIOR FILING DATE: 2000-12-18  
;; PRIOR APPLICATION NUMBER: DE 19961350  
;; PRIOR FILING DATE: 1999-12-17  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-168-185-2

Query Match 63.9%; Score 39; DB 14; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1e+06;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQPMH 9  
Db 1 SVSEIQPMH 9

RESULT 10  
US-10-168-185-8  
;; Sequence 8, Application US/10168185  
;; Publication No. US20030175802A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Armbruster, Franz Paul  
;; APPLICANT: Missbichler, Albert  
;; APPLICANT: Schmidt-Gayk, Heinrich  
;; APPLICANT: Roth, Heinz-Jürgen  
;; TITLE OF INVENTION: Method for Determining Parathormone  
;; FILE REFERENCE: HLZ-004US  
;; CURRENT APPLICATION NUMBER: US/10/168,185  
;; PRIOR FILING DATE: 2002-06-17  
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911  
;; PRIOR FILING DATE: 2000-12-18  
;; PRIOR APPLICATION NUMBER: DE 19961350  
;; PRIOR FILING DATE: 1999-12-17  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 8  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-168-185-8

Query Match 60.7%; Score 37; DB 14; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SEIQPMHN 10  
Db 1 SEIQPMHN 8

RESULT 11  
US-10-192-673-6  
;; Sequence 6, Application US/10192673  
;; Publication No. US20030166838A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gardella, Thomas J.  
;; APPLICANT: Kronenberg, Henry  
;; APPLICANT: Potts, John T.  
;; APPLICANT: Juppner, Harald  
;; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
;; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
;; TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)  
;; FILE REFERENCE: 0609.4570002  
;; CURRENT APPLICATION NUMBER: US/10/192,673  
;; PRIOR FILING DATE: 2002-07-11  
;; PRIOR APPLICATION NUMBER: U.S. 09/421,379

PRIOR FILING DATE: 1999-10-20  
PRIOR APPLICATION NUMBER: U.S. 60/105,530  
PRIOR FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-192-673-6

Query Match 59.0%; Score 36; DB 14; Length 9;  
Best Local Similarity 77.8%; Pred. No. 1e+06;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9  
DB 1 AVSEIQLMH 9

RESULT 12  
US-10-192-673-7  
Sequence 7, Application US/10192673  
Publication No. US20030166838A1  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)  
FILE REFERENCE: 0609.4570002  
CURRENT APPLICATION NUMBER: US/10/192,673  
CURRENT FILING DATE: 2002-07-11  
PRIOR APPLICATION NUMBER: U.S. 09/421,379  
PRIOR FILING DATE: 1999-10-20  
PRIOR APPLICATION NUMBER: U.S. 60/105,530  
PRIOR FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-192-673-7

Query Match 54.1%; Score 33; DB 14; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9  
DB 1 AVSEIQLMH 9

RESULT 13  
US-10-168-165-3  
Sequence 3, Application US/10168185  
Publication No. US20030175802A1  
GENERAL INFORMATION:  
APPLICANT: Armbruster, Franz Paul  
APPLICANT: Misbichler, Albert  
APPLICANT: Schmidt-Gayk, Heinrich  
APPLICANT: Rott, Heinz-Ulrich  
TITLE OF INVENTION: Method for Determining Parathormone  
TITLE OF INVENTION: Activity in a Human Sample

FILE REFERENCE: HLZ-0040US  
CURRENT APPLICATION NUMBER: US/10/168,185  
CURRENT FILING DATE: 2002-06-17  
PRIOR APPLICATION NUMBER: PCT/EP00/12911  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: DE 19961350  
PRIOR FILING DATE: 1999-12-17  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-168-165-3

Query Match 50.8%; Score 31; DB 14; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 8  
DB 1 SVSEIQLMH 8

RESULT 14  
US-10-192-673-10  
Sequence 10, Application US/10192673  
Publication No. US20030166838A1  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)  
FILE REFERENCE: 0609.4570002  
CURRENT APPLICATION NUMBER: US/10/192,673  
CURRENT FILING DATE: 2002-07-11  
PRIOR APPLICATION NUMBER: U.S. 09/421,379  
PRIOR FILING DATE: 1999-10-20  
PRIOR APPLICATION NUMBER: U.S. 60/105,530  
PRIOR FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-192-673-10

Query Match 47.5%; Score 29; DB 14; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9  
DB 1 SVSEIQLMH 9

RESULT 15  
US-10-033-741-61  
Sequence 61, Application US/10033741  
Publication No. US20030049640A1  
GENERAL INFORMATION:  
APPLICANT: Herman, et al.  
TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Vasc  
TITLE OF INVENTION: Response  
FILE REFERENCE: 9195-079  
CURRENT APPLICATION NUMBER: US/10/033,741



Tue May 18 12:03:04 2004

us-09-730-174a-4.closed.rapb

Page 5

;  
; CURRENT FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 61  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-033-741-61

Query Match 44.3%; Score 27; DB 14; Length 10;  
Best Local Similarity 55.6%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIOFMH 9  
|||:  
Db 1 SVSELPVH 9

Search completed: May 18, 2004, 10:20:59  
Job time : 33.25 secs

Tue May 18 12:03:03 2004

us-09-730-174a-4.closed.rat

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:58:45 ; Search time 12.75 Seconds  
(without alignments)

48,589 Million cell updates/sec

Title: US-09-730-174A-4

Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	75.4	12	4	US-09-442-989-31
2	45	73.8	10	3	US-08-817-547A-1
3	39	63.9	9	3	US-08-817-547A-2
4	36	59.0	9	4	US-09-421-379-6
5	33	54.1	9	4	US-09-421-379-7
6	31	50.8	8	3	US-08-817-547A-3
7	29	47.5	9	4	US-09-421-379-10
8	29	47.5	12	2	US-08-140-137A-42
9	28	45.9	11	6	5460978-3
10	26	42.6	6	3	US-08-817-547A-5
11	26	42.6	7	3	US-08-817-547A-4
12	26	42.6	9	4	US-09-421-379-8
13	25	41.0	12	2	US-08-482-228-42
14	25	41.0	12	3	US-08-482-228-42
15	24	39.3	5	2	US-08-177-109A-56
16	24	39.3	5	2	US-08-667-706-56
17	24	39.3	5	3	US-08-817-547A-17
18	24	39.3	6	3	US-08-817-547A-16
19	24	39.3	7	3	US-08-817-547A-15
20	24	39.3	8	2	US-08-748-021-64
21	24	39.3	8	3	US-08-817-547A-14
22	24	39.3	8	3	US-08-974-297-64
23	24	39.3	9	3	US-08-817-547A-13
24	24	39.3	10	3	US-08-817-547A-7
25	23	37.7	9	1	US-07-822-043-26
26	23	37.7	9	1	US-08-346-455B-26
27	23	37.7	9	3	US-08-977-221-26

28	23	37.7	9	4	US-09-483-831B-26	Sequence 26, Appl
29	23	37.7	9	5	PCT-US95-06613-26	Sequence 26, Appl
30	23	37.7	10	2	US-08-116-778B-9	Sequence 9, Appl
31	23	37.7	10	2	US-08-438-562-9	Sequence 9, Appl
32	23	37.7	10	2	US-08-483-528B-97	Sequence 97, Appl
33	23	37.7	10	3	US-08-783-853A-12	Sequence 49, Appl
34	23	37.7	10	3	US-08-836-561-49	Sequence 12, Appl
35	23	37.7	10	3	US-09-280-028-12	Sequence 12, Appl
36	23	37.7	10	4	US-09-344-050-12	Sequence 108, Appl
37	23	37.7	10	4	US-09-393-385B-108	Sequence 49, Appl
38	23	37.7	10	4	US-09-434-122-49	Sequence 3, Appl
39	23	37.7	11	4	US-09-091-071-3	Sequence 61, Appl
40	23	37.7	11	4	US-09-556-605-61	Sequence 1, Appl
41	23	37.7	12	3	US-09-064-750-1	Sequence 60, Appl
42	23	37.7	12	4	US-09-556-605-60	Sequence 83, Appl
43	22	36.1	10	1	US-08-615-181-83	Sequence 2, Appl
44	22	36.1	10	1	US-08-555-579-2	Sequence 14, Appl
45	22	36.1	10	2	US-08-428-257A-14	

#### ALIGNMENTS

RESULT 1  
US-09-442-989-31  
Sequence 31, Application US/09442989  
Parent No. 6569893  
GENERAL INFORMATION:  
APPLICANT: Sledeski, Adam W.  
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC  
FILE REFERENCE: A3113B-US  
CURRENT FILING DATE: 1999-11-18  
EARLIER APPLICATION NUMBER: 60/081,897  
EARLIER FILING DATE: 1998-04-15  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 31  
LENGTH: 12  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)  
OTHER INFORMATION: FMOC-Ala  
NAME/KEY: PEPTIDE  
LOCATION: (3)  
OTHER INFORMATION: Ser(OcBu)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (4)  
OTHER INFORMATION: Glu(OcBu)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (6)  
OTHER INFORMATION: Glu(Trt)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (9)  
OTHER INFORMATION: His(Trt)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (10)  
OTHER INFORMATION: Asn(Trt)  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (8)  
OTHER INFORMATION: Nle  
US-09-442-989-31

Tue May 18 12:03:03 2004

us-09-730-174a-4.closed.ra1

Page 2

Query Match 75.4%; Score 46; DB 4; Length 12;  
Best Local Similarity 75.0%; Pred. No. 0.013;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 SVSEIQFMHNG 12  
1 AVSEIQXHNLS 12  
DB 1 AVSEIQXHNLS 12

RESULT 2  
US-08-817-547A-1  
Sequence 1, Application US/08817547A  
Patent No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Ademann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Maserlein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-817-547A-1

Query Match 73.8%; Score 45; DB 3; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 10  
1 SVSEIQXHN 10  
DB 1 SVSEIQXHN 10

RESULT 3  
US-08-817-547A-2  
Sequence 2, Application US/08817547A  
Patent No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Ademann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Maserlein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence

NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-817-547A-2

Query Match 63.9%; Score 39; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 3e-05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9  
1 SVSEIQXHN 9  
DB 1 SVSEIQXHN 9

RESULT 4  
US-09-421-379-6  
Sequence 6, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
FILE REFERENCE: 0609.4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 6  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-421-379-6

Tue May 18 12:03:03 2004

us-09-730-174a-4.closed.rai

Page 3

Query Match 59.0%; Score 36; DB 4; Length 9;  
Best Local Similarity 77.8%; Pred. No. 3e+05;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 SVSEIQFMH 9  
DB 1 AVSEIQQLMH 9

RESULT 5  
US-09-421-379-7  
Sequence 7, Application US/09421379

PATENT No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
FILE REFERENCE: 0609.4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-421-379-7

Query Match 54.1%; Score 33; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SVSEIQFMH 9  
DB 1 AVSEIQQLMH 9

RESULT 6  
US-08-817-547A-3  
Sequence 3, Application US/08817547A

PATENT No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Adermann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Magerlein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-817-547A-3

Query Match 50.8%; Score 31; DB 3; Length 8;  
Best Local Similarity 87.5%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SVSEIQFMH 8  
DB 1 SVSEIQQLM 8

RESULT 7  
US-09-421-378-10

Sequence 10, Application US/09421379  
PATENT No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
FILE REFERENCE: 0609.4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-421-378-10

Query Match 47.5%; Score 29; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SVSEIQFMH 9  
DB 1 SVSEIQQLMH 9

RESULT 8  
US-08-140-137A-42  
Sequence 42, Application US/08140137A

PATENT No. 5817617  
GENERAL INFORMATION:  
APPLICANT: TUOMANEN, ELAINE  
APPLICANT: MASURE, H. R.

Tue May 18 12:03:03 2004

us-09-730-174a-4.closed.ra1

Page 4

;; TITLE OF INVENTION: ANALOGS OF ENDOTHELIAL LEUCOCYTE  
;; TITLE OF INVENTION: ADHESION MOLECULE (ELAM)  
;; NUMBER OF SEQUENCES: 49  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Klaubner & Jackson  
;; STREET: 411 Hackensack Avenue  
;; CITY: Hackensack  
;; STATE: New Jersey  
;; COUNTRY: USA  
;; ZIP: 07601  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/140,137A  
;; FILING DATE: 27-MAY-1994  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Jackson Esq., David A.  
;; REGISTRATION NUMBER: 26,742  
;; REFERENCE/DOCKET NUMBER: 600-1-096  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201 487-5800  
;; TELEFAX: 201 343-1684  
;;  
;; INFORMATION FOR SEQ ID NO: 42:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; DESCRIPTION: CARD peptide sequence  
;;  
US-08-140-137A-42

Query Match 47.5%; Score 29; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 23;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVSEIQFMH 9  
: || || || ||  
Db 5 ISEBQFVH 12

RESULT 9  
5460978-3  
; Patent No. 5460978  
; APPLICANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,  
; BRUCE E.; WETTENHALL, RICHARD E.H.  
; TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL  
; HYPERCALCEMIA OF MALIGNANCY-PTRHP  
; NUMBER OF SEQUENCES: 4  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/715,280  
; FILING DATE: 14-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 199,235  
; FILING DATE: 09-MAY-1988  
; APPLICATION NUMBER:  
; FILING DATE:  
; SEQ ID NO:3:  
; LENGTH: 11  
5460978-3

Query Match 45.3%; Score 28; DB 6; Length 11;  
Best Local Similarity 60.0%; Pred. No. 32;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 SVSEIQFMH 10  
: || || || || ||  
Db 1 AVSEHOLEHN 10

RESULT 10  
US-08-817-547A-5  
; Sequence 5, Application US/08817547A  
; Patent No. 6030790  
; GENERAL INFORMATION:  
; APPLICANT: Adermann, Knut  
; APPLICANT: Hock, Dieter  
; APPLICANT: Magerlein, Markus  
; TITLE OF INVENTION: Peptides from the hPTH Sequence  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew, LLP  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/817,547A  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/EP95/03757  
;; FILING DATE: 29 SEPT 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: FROST, ROGER T.  
;; REGISTRATION NUMBER: 22,176  
;; REFERENCE/DOCKET NUMBER: 07826-0007  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 404-818-3700  
;; TELEFAX: 404-818-3799  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; HYPOTHEICAL: no  
;; ANTI-SENSE: no  
;;  
US-08-817-547A-5

Query Match 42.6%; Score 26; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQ 6  
: || || || || ||  
Db 1 SVSEIQ 6

RESULT 11  
US-08-817-547A-4  
; Sequence 4, Application US/08817547A  
; Patent No. 6030790  
; GENERAL INFORMATION:  
; APPLICANT: Adermann, Knut  
; APPLICANT: Hock, Dieter  
; APPLICANT: Magerlein, Markus  
; TITLE OF INVENTION: Peptides from the hPTH Sequence  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew, LLP  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-817-547A-4

Query Match 42.6%; Score 26; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQ 6  
DB 1 SVSEIQ 6

RESULT 12  
US-09-421-379-8  
Sequence 8, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (FTHRP)  
FILE REFERENCE: 0609.4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 8  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: peptide  
US-09-421-379-8

Query Match 42.6%; Score 26; DB 4; Length 9;  
Best Local Similarity 55.6%; Pred. No. 3e+05;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9  
DB 1 AVSEHQQLH 9

RESULT 13  
US-08-482-228-42  
Sequence 42, Application US/08482228  
Patent No. 5968753  
GENERAL INFORMATION:

APPLICANT: Tseng-Law, Janet  
APPLICANT: Kobori, Joan A.  
APPLICANT: Al-Abdaly, Fahad A.  
APPLICANT: Guillermo, Roy L.  
APPLICANT: Helgeson, Sam L.  
APPLICANT: Deans, Robert J.  
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL  
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE  
NUMBER OF SEQUENCES: 215  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janice Guthrie, Ph.D.  
STREET: P.O. Box 15210  
CITY: Irvine  
STATE: California  
COUNTRY: USA  
ZIP: 92713-5210

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,228  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Guthrie, Janice  
REGISTRATION NUMBER: 35,170  
REFERENCE/DOCKET NUMBER: IT-4630CIP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 440-5353  
TELEFAX: (714) 553-1952  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-228-42

Query Match 41.0%; Score 25; DB 2; Length 12;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SEIQFMH 9  
DB 5 SSVTFMH 11

RESULT 14  
US-08-482-528-42  
Sequence 42, Application US/08482528  
Patent No. 6017719  
GENERAL INFORMATION:  
APPLICANT: Tseng-Law, Janet  
APPLICANT: Kobori, Joan A.  
APPLICANT: Al-Abdaly, Fahad A.  
APPLICANT: Guillermo, Roy L.  
APPLICANT: Helgeson, Sam L.  
APPLICANT: Deans, Robert J.  
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL  
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE  
NUMBER OF SEQUENCES: 215  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janice Guthrie, Ph.D.  
STREET: P.O. Box 15210

CITY: Irvine  
STATE: California  
COUNTRY: USA  
ZIP: 92713-5210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,528  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Guthrie, Janice  
REGISTRATION NUMBER: 35,170  
REFERENCE/DOCKET NUMBER: IT-4630CIP4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 440-5353  
TELEFAX: (714) 553-1952  
INFORMATION FOR SEQ. ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-528-42

Query Match 41.0%; Score 25; DB 3; Length 12;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SEIQFMH 9  
DB 5 SSVTFMH 11

RESULT 15  
US-08-177-109A-56  
Sequence 56, Application US/08177109A  
Patent No. 586815  
GENERAL INFORMATION:  
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby  
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/177,109A  
FILING DATE: 03-JAN-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: WU 107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ. ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO  
US-08-177-109A-56

Query Match 39.3%; Score 24; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MENLG 12  
DB 1 LNNNG 5

Search completed: May 18, 2004, 10:06:44  
Job time: 13.75 secs

Tue May 18 12:03:08 2004

US-09-730-174a-5.closed.rpr

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:56:10 ; Search time 10.25 seconds  
(without alignments)  
112.614 Million cell updates/sec

Title: US-09-730-174a-5  
Perfect score: 59  
Sequence: 1 AVSEIQLMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1561

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	35.6	12	2	S21205
2	18	30.5	7	2	A58718
3	18	30.5	9	2	S78420
4	18	30.5	10	2	A60589
5	18	30.5	10	2	B46453
6	18	30.5	12	2	A55837
7	17	28.8	7	2	I46868
8	17	28.8	10	2	A37268
9	17	28.8	12	2	PH1190
10	17	28.8	12	2	PH1187
11	17	28.8	12	2	PH1189
12	16	27.1	10	2	A47364
13	16	27.1	11	2	PH0924
14	15	25.4	7	2	S25266
15	15	25.4	7	2	S29735
16	15	25.4	9	2	PM0002
17	15	25.4	9	2	A56029
18	15	25.4	10	2	E49033
19	15	25.4	11	2	A38841
20	15	25.4	11	2	B41835
21	15	25.4	11	2	A40795
22	14	23.7	4	2	I38888
23	14	23.7	7	2	T09512
24	14	23.7	9	2	PT0238
25	14	23.7	10	1	SPGNK
26	14	23.7	10	1	S28055
27	14	23.7	10	2	S27873
28	14	23.7	10	2	C61033
29	14	23.7	11	2	S71304

30	14	23.7	11	2	S60354
31	14	23.7	11	2	B29806
32	14	23.7	11	4	S41909
33	14	23.7	12	2	S25485
34	14	23.7	12	2	G49410
35	14	23.7	12	2	S71034
36	14	23.7	12	2	PH1175
37	14	23.7	12	2	PH1174
38	14	23.7	12	2	I41235
39	13	22.0	6	2	PQ0008
40	13	22.0	8	2	T14906
41	13	22.0	8	2	JS0316
42	13	22.0	8	2	PH1618
43	13	22.0	9	2	S13636
44	13	22.0	9	2	UN0026
45	13	22.0	9	2	PT0231

retinal oxidase -  
acidic proline-rich  
hypothetical prote  
transcription fact  
t-complex polypept  
pote protein - Sal  
T-cell receptor al  
T-cell receptor al  
glutamine-tRNA lig  
angiotensin-conver  
hypothetical prote  
leucokinin VI - Ma  
Ig H chain V-D-J r  
coat protein beta  
specm-activating p  
Ig heavy chain CDR

#### ALIGNMENTS

RESULT 1  
S21205  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C/Accession: S21205  
R/Makiya, R./ Stigbrand, T.  
Eur. J. Biochem. 205, 341-345, 1992  
A/Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin  
A/Reference number: S21205; PMID:92209522; PMID:1555592  
A/Accession: S21205  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12 <MA>  
C/Keywords: heterotrimer; immunoglobulin

Query Match 35.6%; Score 21; DB 2; Length 12;  
Best Local Similarity 44.4%; Pred. No. 6.9e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 EIQLMHNLG 12  
Db 1 EVOLVESGG 9

RESULT 2  
A58718  
carnocin U149 - Carnobacterium sp. (fragment)  
C/Species: Carnobacterium sp.  
C/Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998  
C/Accession: A58718  
R/Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Hojo, H.; Nes, I.F.  
Appl. Environ. Microbiol. 58, 1417-1422, 1992  
A/Title: Purification and characterization of a new bacteriocin isolated from a Carnobac  
A/Reference number: A58718; PMID:92321768; PMID:1622206  
A/Accession: A58718  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <STO>  
C/Keywords: antibiotic; lanthionine

Query Match 30.5%; Score 18; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6  
Db 2 SEIQ 5

RESULT 3  
S78420



ribosomal protein RL41, mitochondrial [validated] - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)  
C/Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #ext\_change 21-Jul-2000

A/Accession: S78420  
R/Soldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998  
A/Reference number: S78411

A/Accession: S78420  
A/Molecule type: protein

A/Residues: 1-9 <GOL>

A/Note: the protein is designated as mitochondrial ribosomal protein L41  
C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match  
Best Local Similarity 30.5%; Score 18; DB 2; Length 9;  
Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12

DB 5 HRLG 8

#### RESULT 4

A/Accession: A60589  
sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SNP-I) - slate-pencil urchi

C/Species: Heterocentrotus mammillatus  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #ext\_change 18-Aug-2000

A/Accession: A60589  
R/Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi

Comp. Biochem. Physiol. B 94, 739-751, 1989  
A/Title: A halogenated amino acid-containing sperm activating peptide and its related pe

ptide mndus; Echinometrina machaei and Heterocentrotus mammillatus.

A/Reference number: A60527  
A/Accession: A60589

A/Molecule type: protein  
A/Residues: 1-10 <YOS>

C/Superfamily: unassigned animal peptides

Query Match  
Best Local Similarity 30.5%; Score 18; DB 2; Length 10;  
Pred. No. 2.1e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNLG 12

DB 2 YNLG 5

#### RESULT 5

A/Accession: B46453  
e antigen p20e precursor - hepatitis B virus (subtype adr) (fragment)

N/Alternate names: HBe antigen precursor  
N/Contains: e antigen

C/Species: hepatitis B virus, HBV  
A/Variety: subtype adr

C/Date: 18-Jun-1993 #sequence\_revision 08-Nov-1996 #ext\_change 15-Aug-1997  
R/Takahashi, K.; Kishimoto, S.; Ohori, K.; Yoshizawa, H.; Machida, A.; Ohnuma, H.; Tsuda

J. Immunol. 147, 3156-3160, 1991  
A/Title: Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepa

A/Reference number: A46453; MUID:92013147; PMID:1717588

A/Accession: B46453  
A/Status: preliminary

A/Molecule type: protein  
A/Residues: 1-10 <TK>

A/Experimental source: subtype adr  
A/Note: sequence extracted from NCBI backbone (NCBI:60243)

F,1-10/Domain: signal sequence (fragment) #status predicted <SIG>

Query Match  
Best Local Similarity 30.5%; Score 18; DB 2; Length 10;  
Pred. No. 2.1e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 IOLMH 9

DB 1 MOLFH 5

#### RESULT 6

A/Accession: A55837  
5-aminimidazole ribonucleotide carboxylase/4-N-succinylamino carbonyl-5-aminimidazole

C/Species: Gallus gallus (chicken)  
C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #ext\_change 17-Mar-1999

A/Accession: A55837  
R/Firestone, S.M.; Davison, V.J.

Biochemistry 33, 11917-11926, 1994  
A/Title: Carboxylases in de Novo purine biosynthesis. Characterization of the Gallus gal

A/Reference number: A55837; MUID:95001903; PMID:7918410

A/Accession: A55837  
A/Status: preliminary

A/Molecule type: protein  
A/Residues: 1-12 <FIR>

Query Match  
Best Local Similarity 30.5%; Score 18; DB 2; Length 12;  
Pred. No. 2.6e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVEFIOL 7

DB 2 AASLAL 8

#### RESULT 7

A/Accession: 146868  
alpha-myosin heavy chain - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #ext\_change 05-Nov-1999

A/Accession: 146868  
R/Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.

Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984  
A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula

A/Reference number: 146868; MUID:84221901; PMID:6328491

A/Accession: 146868  
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA  
A/Residues: 1-7 <FRI>

A/Cross-references: GB:X01698; NID:g165538; PIDN:AAA11415.1; PID:g165539

Query Match  
Best Local Similarity 28.8%; Score 17; DB 2; Length 7;  
Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QLMHN 10

DB 1 QXKMD 5

#### RESULT 8

A/Accession: A37268  
1g heavy chain C region (129) - mouse (fragment)

C/Species: Mus musculus (house mouse)  
C/Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #ext\_change 13-Mar-1998

A/Accession: A37268  
R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991  
A/Title: Heavy and light chain variable region sequences and antibody properties of anti

A/Reference number: A37268; MUID:91177923; PMID:1706720

A/Accession: A37268  
A/Status: preliminary

A/Molecule type: mRNA  
A/Residues: 1-10 <RUF>

Query Match  
Best Local Similarity 28.8%; Score 17; DB 2; Length 10;  
Pred. No. 3.3e+03;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQLMHNLG 12

Db 1 ESQSFNNVG 9

## RESULT 9

PH1190  
T-cell receptor alpha chain V region (CW3/10.1) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1190  
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
J. Exp. Med. 176, 439-447, 1992  
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A/Reference number: S26512; MUID:92364546; PMID:1380061  
A/Accession: PH1190  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-12 <CAS>

Query Match 28.8%; Score 17; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSE 4  
|||  
Db 2 AVSE 5

## RESULT 10

PH1187  
T-cell receptor alpha chain V region (CW3/1F11) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1187  
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
J. Exp. Med. 176, 439-447, 1992  
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A/Reference number: S26512; MUID:92364546; PMID:1380061  
A/Accession: PH1187  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-12 <CAS>

Query Match 28.8%; Score 17; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSE 4  
|||  
Db 2 AVSE 5

## RESULT 11

PH1189  
T-cell receptor alpha chain V region (CW3/2C3) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1189  
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
J. Exp. Med. 176, 439-447, 1992  
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A/Reference number: S26512; MUID:92364546; PMID:1380061  
A/Accession: PH1189  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-12 <CAS>

Query Match 28.8%; Score 17; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSE 4  
|||

Db 2 AVSE 5

## RESULT 12

A47364  
Placental lactogen-I precursor - mouse (fragment)  
C/Species: Mus sp. (mouse)  
C/Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
C/Accession: A47364  
R/Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.  
Mol. Endocrinol. 7, 181-188, 1993  
A/Title: Trophoblast-specific transcription from the mouse placental lactogen-I gene pro  
A/Reference number: A47364; MUID:93225959; PMID:8469232  
A/Accession: A47364  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-10 <RES>  
A/Cross-references: GB:S58124; NID:9299449

Query Match 27.1%; Score 16; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 5.1e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IOLMHNL 11  
|||  
Db 1 MOLTNL 7

## RESULT 13

PH0924  
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C/Accession: PH0924  
R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy  
A/Reference number: PH0924; MUID:92078857; PMID:1836012  
A/Accession: PH0924  
A/Molecule type: mRNA  
A/Residues: 1-11 <GOL>  
A/Experimental source: concanavalin A-activated lymphoblast  
C/Keywords: T-cell receptor

Query Match 27.1%; Score 16; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 5.7e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIQLM 8  
|||  
Db 2 ASSGMDLM 9

## RESULT 14

S25266  
p11E protein - Escherichia coli (fragment)  
C/Species: Escherichia coli  
C/Date: 28-May-1993 #sequence\_revision 28-May-1993 #text\_change 11-Jun-1993  
C/Accession: S25266  
R/Dubuy, B.; Taha, M.K.; Rosset, O.; Marchal, C.; Pugsley, A.P.  
Mol. Microbiol. 6, 1887-1894, 1992  
A/Title: p11E, a component of the pullulanase secretion pathway of Klebsiella oxytoca, C  
A/Reference number: S25266; MUID:92374839; PMID:1354853  
A/Accession: S25266  
A/Molecule type: protein  
A/Residues: 1-7 <DUP>  
C/Genetics:  
A/Gene: p11E

Query Match 25.4%; Score 15; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IOLM 8  
|:|  
Db 4 IELM 7

## RESULT 15

S29735  
polyphosphate-glucose phosphotransferase (EC 2.7.1.63) - *Propionibacterium freudenreichii*  
C;Species: *Propionibacterium freudenreichii* subsp. *shermanii*  
C;Date: 19-Mar-1997 #sequence\_rev19-MAR-1997 #text\_change 03-Jun-2002  
C;Accession: S29735  
R;Phillips, N.F.B.; Horn, P.J.; Wood, H.G.  
Arch. Biochem. Biophys. 300, 309-319, 1993  
A;Title: The polyphosphate- and ATP-dependent glucokinase from *Propionibacterium shermanii*  
A;Reference number: S29735; MWID:93143332; PMID:8380966  
A;Accession: S29735  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <PHI>  
C;Keywords: phosphotransferase

Query Match 25.4%; Score 15; DB 2; length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12  
|:|  
Db 2 HVLG 5

Search completed: May 18, 2004, 10:05:41  
Job time : 11.25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:43:45 ; Search time 6.75 Seconds  
(without alignments)

92.569 Million cell updates/sec

Title: US-09-730-174a-5  
Perfect score: 59  
Sequence: 1 AVSEIQLMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141661 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	# Query	Length	ID	Description
1	18	30.5	7	1	LANC_CARUT
2	16	27.1	8	1	ALB6_CYPPO
3	16	27.1	8	1	FUS5_FUSSO
4	16	27.1	11	1	EBG_CLOPA
5	15	25.4	11	1	PKKI_PPRAM
6	14	23.7	6	1	TRPI_PSPPU
7	14	23.7	7	1	AL17_CVDPO
8	14	23.7	8	1	AL18_CARMA
9	14	23.7	8	1	AL11_CVDPO
10	14	23.7	9	1	FAR8_MACRS
11	14	23.7	9	1	UF02_MOUSE
12	14	23.7	10	1	AL19_CARMA
13	14	23.7	10	1	PSBF_CAPAN
14	14	23.7	10	1	TEMK_PANTE
15	14	23.7	10	1	TKNC_RANCA
16	14	23.7	10	1	TKNK_PTC
17	14	23.7	11	1	ASL1_BACSE
18	14	23.7	12	1	CD14_LITXA
19	14	23.7	12	1	CD14_LITXA
20	14	23.7	12	1	POPD_MERTM
21	14	23.7	12	1	RS19_TOSBP
22	14	22.0	8	1	LCK4_LEBMA
23	13	22.0	8	1	LCK6_LEBMA
24	13	22.0	9	1	WOSH_CLYXA
25	13	22.0	9	1	PPKI_PPRAM
26	13	22.0	10	1	RRPL_PPRAM
27	13	22.0	11	1	CS15_BACSU
28	13	22.0	11	1	O20A_COMTE
29	13	22.0	12	1	PPK4_PPRAM
30	12	20.3	9	1	FIB3_PAPHA
31	12	20.3	9	1	RE42_LITRU
32	12	20.3	10	1	GLEM_HUMAN
33	12	20.3	10	1	GONI_CUTPA

34	12	20.3	10	1	GON2_CHEPR
35	12	20.3	10	1	HTR1_ROWMI
36	12	20.3	10	1	HTE_HELZE
37	12	20.3	10	1	SVK_CAMUP
38	12	20.3	10	1	TKNE_RANR1
39	12	20.3	11	1	CXL1_CONMR
40	12	20.3	11	1	HS70_PINPS
41	12	20.3	11	1	TZP1_PROTU
42	12	20.3	12	1	HEP1_BACSE
43	12	20.3	12	1	PPK4_PPRAM
44	11	18.6	7	1	TY51_LITRU
45	11	18.6	7	1	UN06_PINPS

## ALIGNMENTS

RESULT 1  
ID LANC\_CARUT STANDARD; PRT; 7 AA.  
AC P16560; 1  
DT 01-JUN-1994 (Rel. 29, Created)  
DE 01-JUN-1994 (Rel. 29, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lantibiotic carnocin U149 (Fragment).  
OS Carnobacterium sp. (strain U149).  
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
OC Carnobacterium.  
OK NCBI\_TaxID=35782;  
RN [1]  
RP MEDLINE=92321768; Pubmed=1622206;  
RX Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
Nes I.F.;  
RT "Purification and characterization of a new bacteriocin isolated from  
a Carnobacterium sp.";  
RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
CC -1- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).  
CC Active on Gram-positive bacteria.  
KW Antibiotic; Bacteriocin; Lantibiotic.  
KW NON TER  
FT SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 30.5%; Score 18; DB 1; Length 7;  
Best local similarity 100.0%; Pred. No. 1.4e-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6  
|||  
Db 2 SEIQ 5

RESULT 2  
ID AL16\_CVDPO STANDARD; PRT; 8 AA.

AC P82157; 1  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydiaastatin 6.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
OC NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; Pubmed=9392829;  
RA Duvé H., Johnsen A.H., Maestre J.-L., Scott A.G., Winstanley D.,  
Davy M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily.";  
RL Peptides 18:1301-1309(1997).

CC -1- SIMILARITY: Belongs to the allostatin family.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 27.1%; Score 16; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MHNLG 12  
 Db 3 LYNFG 7

RESULT 3  
 FUSS\_FUSSO STANDARD; PRT; 8 AA.  
 ID FUSS\_FUSSO  
 AC P81010;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Allergen Fus s 13596\* (Fragment).  
 OS Fusarium solani (subsp. pisi) (Nectria haematococca).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 CC Hypocreomycetidae; Hypocerales; Nectriaceae; Nectria.  
 RX NCBI\_TaxID=70791;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=IARI 3596; TISSUE=Mycelium;  
 RA Verma J.; Gangal S.V.;  
 RL Submitted (JUL-1997) to Swiss-Prot.  
 CC -1- ALLERGEN: Causes an allergic reaction in human.  
 KW Allergen.  
 FT NON TER  
 SQ SEQUENCE 8 AA; 898 MW; C372C441F5B65041 CRC64;

Query Match 27.1%; Score 16; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMNL 11  
 Db 3 MSHNV 7

RESULT 4  
 ERG\_CLOPA STANDARD; PRT; 11 AA.  
 ID ERG\_CLOPA  
 AC P81350;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Elongation factor G (EF-G) (CP 5) (Fragment).  
 GN FUSA.  
 OS Clostridium pasteurianum.  
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 RX NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=MS;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Flensburg R.; Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis, separation and N-terminal  
 sequence analysis of proteins from Clostridium pasteurianum WS.";  
 RL Electrophoresis 19:802-806(1998).  
 CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of  
 the nascent protein chain from the A-site to the P-site of the  
 ribosome.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.  
 CC EF-G/EF-2 subfamily.  
 DR InterPro; IPR000795; EF\_GTPbind.

DR PROSITE; PS00301; EFACOR\_GTP; PARTIAL.  
 KW Elongation factor; Protein biosynthesis; GTP-binding.  
 FT NON TER 11  
 SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 27.1%; Score 16; DB 1; Length 11;  
 Best Local Similarity 25.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 TQLMHNLG 12  
 Db 4 LEKFNIG 11

RESULT 5  
 PVK1\_PERAM STANDARD; PRT; 11 AA.  
 ID PVK1\_PERAM  
 AC P41837;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Periviscerokinin-1 (Pea-PVK-1).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 RX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE AND SYNTHESIS.  
 RC TISSUE=Abdominal periviscerokinin organs;  
 RA MEDLINE=95232021; PubMed=7716075;  
 RA Predel R.; Linde D.; Rapus D.; Vettermann S.; Penzlin H.;  
 RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the  
 periviscerokinin organs of the American cockroach.";  
 RL Peptides 16:61-66(1995).  
 CC -1- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE  
 HYPERNEURAL MUSCLE.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 11  
 SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 25.4%; Score 15; DB 1; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 TQLMHN 10  
 Db 6 IPVMRN 11

RESULT 6  
 TRPI\_PSEPU STANDARD; PRT; 6 AA.  
 ID TRPI\_PSEPU  
 AC P36414;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE HTH-type transcriptional regulator trpi (TrpBA operon transcriptional  
 activator) (Fragment).  
 GN TRPI.  
 OS Pseudomonas putida.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 RX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PPG1 C18;  
 RX MEDLINE=89335826; PubMed=2503057;  
 RA Eberly L.; Crawford I.P.;  
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas  
 putida.";  
 RL Biochimie 71:521-531(1999).  
 CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING

CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE  
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRP1 BINDS UPSTREAM OF THE  
CC TRAP OPERON OVERLAPPING ITS OWN PROMOTER REGION.  
CC -1- SIMILARITY: Contains 1 HTH lyase-type DNA-binding domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X13299; CAA31660.1; -  
CC InterPro; IPR000847; HTH\_LYER; PARTIAL.  
CC PROSITE; PS50911; HTH\_LYER; PARTIAL.  
CC Tryptophan biosynthesis; Transcription regulation; Activator;  
CC DNA binding.  
CC NON\_TER 6 6  
CC SEQUENCE 6 AA; 683 MW; 77672A1EDD6F000 CRC64;  
CC  
CC Query Match 23.7%; Score 14; DB 1; Length 6;  
CC Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
CC Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 LHMNL 11  
Db 1 MAHDL 5

RESULT 7  
ID ALL7\_CYPDPO STANDARD; PRT; 7 AA.  
AC P82158;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydiastatin 7.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_Taxid=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Davey H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily";  
RL Peptides 18:1301-1309(1997).  
CC -1- SIMILARITY: Belongs to the allatostatin family.  
CC Neuropeptide; Amidation.  
CC MOD\_RES 7  
FT SEQUENCE 7 AA; 873 MW; 672879CAB8569350 CRC64;  
FT

Query Match 23.7%; Score 14; DB 1; Length 7;  
Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 8 MHNLG 12  
Db 2 MYDFG 6

RESULT 8  
ID AL18\_CARMA STANDARD; PRT; 8 AA.  
AC P81821;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 18.

OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Plecymenata; Brachyura;  
OC Brachyura; Portunodea; Portunidae; Carcinus.  
OX NCBI\_Taxid=6759;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Davey H., Johnsen A.H., Maestro J.-L., Scott A.G., Jares P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.  
CC -1- SIMILARITY: Belongs to the allatostatin family.  
CC Neuropeptide; Amidation; Multigene family.  
CC MOD\_RES 8  
FT SEQUENCE 8 AA; 919 MW; C82879D5AB5692A5 CRC64;  
FT

Query Match 23.7%; Score 14; DB 1; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 8 MHNLG 12  
Db 3 MYDFG 7

RESULT 9  
ID ALL1\_CYPDPO STANDARD; PRT; 8 AA.  
AC P82152;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydiastatin 1.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_Taxid=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Davey H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily";  
RL Peptides 18:1301-1309(1997).  
CC -1- SIMILARITY: Belongs to the allatostatin family.  
CC Neuropeptide; Amidation.  
CC MOD\_RES 8  
FT SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;  
FT

Query Match 23.7%; Score 14; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 HNLG 12  
Db 4 YNFG 7

RESULT 10  
ID FAR8\_MACRS STANDARD; PRT; 9 AA.  
AC P83281;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLR8 (VSHNRLRF-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).

```

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=1179812;
RA Sithigorngul P., Sarathongskum W., Longyant S., Pandhan N.,
RA Sithigorngul W., Petsom A.;
RT "Three more novel FMRFamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -1- MASS SPECTROMETRY: MW=1193.8; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR GO:GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RRS 9
SQ SEQUENCE 9 AA; 1133 MW; 845A0729C44441F5 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HN 10
DB 3 HN 4

RESULT 11
UF02_MOUSE STANDARD; PRT; 9 AA.
AC P38640;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.0, its MW is: 32 kDa.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1102 MW; 7573EAB6D05B1AAB CRC64;

Query Match 23.7%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIQ 6
DB 4 EIQ 6

RESULT 12
AL19_CARMA STANDARD; PRT; 10 AA.
AC P81822;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinstatin 19.
OS Carcinus maenas (Common shore crab) (Green crab).

```

```

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Dure H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thore A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -1- SIMILARITY: Belongs to the allatostatin family.
CC Neuropeptide; Amidation; Multigene family.
KW MOD_RRS 10
FT MOD_RRS 10
SQ SEQUENCE 10 AA; 1101 MW; 96687CD5A569A81 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MNING 12
DB 5 MYSFG 9

RESULT 13
PSBF_CAPAN STANDARD; PRT; 10 AA.
AC Q03367;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b559 beta subunit (PSII reaction center subunit VII)
DE (Fragment).
OS Capsicum annuum (Bell pepper).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;
RX MEDLINE=9309270; PubMed=1463853;
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;
RT "The publ gene from bell pepper (Capsicum annuum): plastid RNA
RT editing also occurs in non-photosynthetic chromoplasts.";
RL Plant Mol. Biol. 20:1185-1188(1992).
CC -1- FUNCTION: This D-type cytochrome is tightly associated with the
CC reaction center of photosystem II and possibly is part of the
CC water-oxidation complex.
CC -1- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC -1- SIMILARITY: Belongs to the psbE / psbF family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X65570; CAA46539.1; -
CC F01; S28055; S28055.
CC HAMAP: MF_00643; -; 1.
CC InterPro: IPR006216; Cyt_b559.
CC PROSITE: PS00537; CYTOCHROME_B559; PARTIAL.
CC Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT NON_TER 1

```

FT TRANSMEM <1 5 BY SIMILARITY.  
 FT DOMAIN 6 10 LUMENAL (POTENTIAL).  
 SQ SEQUENCE 10 AA; 1180 MW; 817DOF59D6D9DC5 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;  
 Best Local Similarity 25.0%; Pred. No. 7.7e+03;  
 Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVEFQQLM 8  
 DB 1 SISAMQFI 8

RESULT 14  
 TEMK\_RANCA STANDARD; PRT; 10 AA.  
 AC P56923;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Temporin K.  
 OS Rana temporaria (European common frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 CX NCBI\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97175050; PubMed=9022710;  
 RA Simmaco M., Magnogna G., Canofeni S., Miele R., Mangoni M.L.,  
 RA Barra D.;  
 RT "Temporins, antimicrobial peptides from the European red frog Rana  
 temporaria";  
 RL Eur. J. Biochem. 242:788-792(1996).  
 CC -1- FUNCTION: Has antibacterial activity against Gram-positive  
 CC bacteria.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- SIMILARITY: Belongs to the brevinin family.  
 KM Amphibian defense peptide; Antibiotic; Amidation.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 7.7e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMENL 11  
 DB 1 LLEPL 5

RESULT 15  
 TKNC\_RANCA STANDARD; PRT; 10 AA.

AC P22650;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ranatrichylin C (RTK C).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 CX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Intestine;  
 RX MEDLINE=91254337; PubMed=2041143;  
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)  
 brain and intestine";  
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
 RN [2]

RP SEQUENCE.  
 RC TISSUE=Intestine; PubMed=8210506;  
 RX MEDLINE=94023216; PubMed=8210506;  
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and  
 intestine";  
 RL Regul. Pept. 46:81-88(1993).  
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR: G61033; G61033.  
 DR InterPro: IPR002040; Tachy. Neurokinin.  
 DR PROSITE: PS00267; TACHYKININ, 1.  
 KM Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1086 MW; 3A3A407059D5BDC7 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HN 10  
 DB 1 HN 2

Search completed: May 15, 2004, 10:02:34  
 Job time : 6.75 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:55:20 ; Search time 30.25 Seconds  
(without alignments)  
125.164 Million cell updates/sec

Title: US-09-730-174a-5  
Perfect score: 59  
Sequence: 1 ANSEIQLENNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	27	45.8	11 13	Q9PS71 agkistron
2	23	39.0	12 13	P82081 limodynast
3	20	33.9	8 13	P82082 limodynast
4	20	33.9	8 13	P82083 limodynast
5	20	33.9	12 13	P82085 limodynast
6	19	32.2	8 8	Q34909 locusta mg
7	19	32.2	9 12	Q92766 canine dist
8	19	32.2	9 12	O71066 canine dist
9	18	30.5	8 10	Q40659 cryza sativ
10	18	30.5	10 12	Q9PXC3
11	18	30.5	11 5	Q23876 dictyosteli
12	18	30.5	12 15	Q85631 avian carc
13	17	28.6	7 6	Q28742 oryctolagus
14	17	28.6	9 4	Q15891 homo sapien
15	17	28.6	9 8	Q9GD12 limospadix
16	17	28.6	9 8	Q9GCV6 sclerosperm

17	17	28.8	11 10	P82336	P82336 pistum sativ
18	17	28.8	11 13	Q9PST1	Q9PST1 fugu rubrip
19	16	27.1	8 3	Q05403	Q05403 saccharomyc
20	16	27.1	8 4	Q15894	Q15894 homo sapien
21	16	27.1	9 2	Q44377	Q44377 aeromonas t
22	16	27.1	9 2	Q44468	Q44468 aeromonas v
23	16	27.1	9 2	Q8RKU3	Q8RKU3 borrelia bu
24	16	27.1	9 2	Q43928	Q43928 aeromonas p
25	16	27.1	9 2	Q44001	Q44001 aeromonas e
26	16	27.1	9 2	Q9K4M6	Q9K4M6 staphylococ
27	16	27.1	9 10	Q9FXL0	Q9FXL0 illium long
28	16	27.1	10 2	Q7WUG1	Q7WUG1 pseudomonas
29	16	27.1	10 10	P82132	P82132 spinacia ol
30	16	27.1	10 10	P82133	P82133 spinacia ol
31	16	27.1	10 13	P82080	P82080 limodynast
32	16	27.1	12 2	Q9X6Y0	Q9X6Y0 aquifex pyr
33	15	25.4	7 12	Q66205	Q66205 transistib
34	15	25.4	8 13	P82079	P82079 limodynast
35	15	25.4	9 2	Q43960	Q43960 azotobacter
36	15	25.4	9 5	Q8WRI9	Q8WRI9 dirosophila
37	15	25.4	10 6	Q9TS43	Q9TS43 sus scrofa
38	15	25.4	10 8	Q8WBR7	Q8WBR7 chaltophoru
39	15	25.4	11 6	Q9BDC8	Q9BDC8 pongo pygma
40	15	25.4	11 6	Q9BDQ9	Q9BDQ9 gorilla gor
41	15	25.4	11 6	Q9BDD0	Q9BDD0 pan troglod
42	15	25.4	11 6	Q9BDC9	Q9BDC9 pan paniscu
43	15	25.4	12 6	Q9TQY5	Q9TQY5 bos taurus
44	15	25.4	12 11	Q9ROV3	Q9ROV3 mus musculu
45	14	23.7	8 2	Q49534	Q49534 mycoplasma

## ALIGNMENTS

RESULT 1	Q9PS71	PRELIMINARY;	PRT;	11 AA.
AC	Q9PS71;			
DT	01-MAY-2000 (TREMBlrel. 13, Created)			
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)			
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
DE	Fibrinolytic metalloproteinase (Fragment).			
OS	Agkistrodon contortrix.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae;			
OC	Viperidae; Crotalinae; Agkistrodon.			
OX	NCBI_TaxID=8720;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=91378546; PubMed=1898066;			
RA	Guan A.L., Ketzius A.D., Henderson G.N., Markland F.S.Jr.;			
RT	"Purification and characterization of a fibrinolytic enzyme from venom			
RT	of the southern copperhead snake (Agkistrodon contortrix			
RT	contortrix).";			
RL	Arch. Biochem. Biophys. 289:197-207(1991).			
FT	NON TER			
SO	SEQUENCE	11 AA;	1209 MW;	7CA02D1D41E8772B CRC64;
Query Match		45.8%;	Score 27;	DB 13;
Best Local Similarity		71.4%;	Pred. No. 1.4e+02;	Length 11;
Matches	5;	Conservative	1;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	6 QLMENLG 12			
DB	4 ELGNLIG 10			
RESULT 2	P82081	PRELIMINARY;	PRT;	12 AA.
ID	P82081;			
AC	P82081;			
DT	01-MAY-2000 (TREMBlrel. 13, Created)			
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)			

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 3.  
 OS Limnodynastes terraereginae (Northern banjo frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 CC Limnodynastinae; Limnodynastes.  
 NCBI\_TaxID=104894;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=TIBIAL GLAND;  
 RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 the banjo frogs Limnodynastes interioris, Limnodynastes dumerilii and  
 Limnodynastes terraereginae".  
 RL Aust. J. Chem. 46:833-842(1993).  
 CC -1- MASS SPECTROMETRY: MW=1236; METHOD=FAB.  
 CC SEQUENCE 12 AA; 1236 MW; 147AAV0PDPF472724 CRC64;  
 SQ

Query Match 39.0%; Score 23; DB 13; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 1e+03;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 LMENLG 12  
 : : : :  
 6 LNNLNG 11

RESULT 3  
 ID P82082 PRELIMINARY; PRT; 8 AA.  
 AC P82082;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 4.  
 OS Limnodynastes salmini (Salmin's-striped frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 CC Limnodynastinae; Limnodynastes.  
 NCBI\_TaxID=39404;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri".  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -1- MASS SPECTROMETRY: MW=772; METHOD=FAB.  
 CC SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;  
 SQ

Query Match 33.9%; Score 20; DB 13; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMENLG 12  
 : : : :  
 2 LVSNLG 7

RESULT 4  
 ID P82083 PRELIMINARY; PRT; 8 AA.  
 AC P82083;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 5.  
 OS Limnodynastes salmini (Salmin's-striped frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 CC Limnodynastinae; Limnodynastes.  
 NCBI\_TaxID=39404;  
 RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri".  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -1- MASS SPECTROMETRY: MW=786; METHOD=FAB.  
 CC SEQUENCE 8 AA; 786 MW; 7B58772455B05728 CRC64;  
 SQ

Query Match 33.9%; Score 20; DB 13; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMENLG 12  
 : : : :  
 2 LISNLG 7

RESULT 5  
 ID P82085 PRELIMINARY; PRT; 12 AA.  
 AC P82085;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 7.  
 OS Limnodynastes salmini (Salmin's-striped frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 CC Limnodynastinae; Limnodynastes.  
 NCBI\_TaxID=39404;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri".  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -1- MASS SPECTROMETRY: MW=1114; METHOD=FAB.  
 CC SEQUENCE 12 AA; 1114 MW; 3AB5A976CAA72728 CRC64;  
 SQ

Query Match 33.9%; Score 20; DB 13; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 4.2e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMENLG 12  
 : : : :  
 6 LITNLG 11

RESULT 6  
 ID Q34909 PRELIMINARY; PRT; 8 AA.  
 AC Q34909;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Cytochrome b (Fragment).  
 OS Locusta migratoria (Migratory locust).  
 OG Mitochondrion.  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RX MEDLINE=88223478; PubMed=2836084;  
 RA McCracken A., Unruhscen I., Gellissen G.;  
 RT "Structure of the cloned Locusta migratoria mitochondrial genome:  
 restriction mapping and sequence of its ND-1 (URF-1) gene".  
 RL Curr. Genet. 11:625-630(1987).  
 DR EMBL; X05286; CAA28905.1; "-".  
 DR GO; GO:0005739; Mitochondrion; IEA.

KW Mitochondrion. 1  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;  
Query Match 32.2%; Score 19; DB 8; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1e+06;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 2 VSEIOLMH 9  
DB 1 MSYIKLKH 8  
RESULT 7  
ID 092766 PRELIMINARY; PRT; 9 AA.  
AC 092766;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE Fusion protein (Fragment).  
GN F.  
OC Canine distemper virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
OX NCBI\_TaxID=11232;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Dog #5526/89.  
RA Liemann H., Harder T., Haas L.;  
RT "Genetic analysis of the central untranslated genome region and the  
RT proximal coding part of the F gene of wild-type and vaccine distemper  
RT morbilliviruses."  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF026237; AAC09167.1; -.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;  
Query Match 32.2%; Score 19; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 MEN 10  
DB 1 MHN 3  
RESULT 8  
ID 071066 PRELIMINARY; PRT; 9 AA.  
AC 071066;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Fusion protein (Fragment).  
GN F.  
OC Canine distemper virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
OX NCBI\_TaxID=11232;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Dog #10757/96;  
RA Liemann H., Harder T., Haas L.;  
RT "Genetic analysis of the central untranslated genome region and the  
RT proximal coding part of the F gene of wild-type and vaccine distemper  
RT morbilliviruses."  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF026234; AAC09164.1; -.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;

Query Match 32.2%; Score 19; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 MEN 10  
DB 1 MHN 3  
RESULT 9  
ID 040659 PRELIMINARY; PRT; 8 AA.  
AC 040659;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Alpha-amylase (Fragment).  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=91078641; PubMed=2258052;  
RA Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,  
RA Rodriguez R.L.;  
RT "Expression and secretion of rice alpha-amylase by saccharomycers  
RT cerevisiae."  
RL Gene 94:209-216(1990).  
DR EMBL; M62916; AAA33892.1; -.  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 948 MW; EBC694444732D66 CRC64;  
Query Match 30.5%; Score 18; DB 10; Length 8;  
Best Local Similarity 28.6%; Pred. No. 1e+06;  
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
QY 5 IOLMH 11  
DB 1 MQLNMN 7  
RESULT 10  
ID 09PXC3 PRELIMINARY; PRT; 10 AA.  
AC 09PXC3;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE E antigen P208 (Fragment).  
OS Hepatitis B virus.  
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10407;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92013147; PubMed=1717588;  
RA Takahashi K., Kishimoto S., Ohori K., Yoshizawa H., Machida A.,  
RA Ohnuma H., Tsuda F., Muneoka E., Miyakawa Y., Mayumi M.;  
RT "Molecular heterogeneity of e antigen polypeptides in sera from  
RT carriers of hepatitis B virus."  
RL J. Immunol. 147:3156-3160(1991).  
DR PIR; B46453; B46453.  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1238 MW; 485A6E3AE721B9C7 CRC64;  
Query Match 30.5%; Score 18; DB 12; Length 10;  
Best Local Similarity 60.0%; Pred. No. 8.9e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 5 IOLMH 9

Db 1 MOLF 5

## RESULT 11

Q23876 ID Q23876 PRELIMINARY; PRT; 11 AA.  
 AC Q23876; RT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE Actin 4.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostellum.  
 CX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82260445; PubMed=6286214;  
 RA McKown M., Firtel R.A.;  
 RT "Actin multigene family of Dictyostellum."  
 RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).  
 DR EMBL; K02957; AAA33150.1; JOINED.  
 DR EMBL; K02956; AAA33150.1; JOINED.  
 SQ SEQUENCE 11 AA; 1205 MW; 728B4C14C6C2CAAB CRC64;

Query Match 30.5%; Score 18; DB 5; Length 11;  
 Best Local Similarity 28.6%; Pred. No. 9.9e+03;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 EIOGMN 10  
 Db 5 DVQALNN 11

## RESULT 12

Q85631 ID Q85631 PRELIMINARY; PRT; 12 AA.  
 AC Q85631; RT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE MH2, proviral DNA, myc to 3' LTR (Fragment).  
 OS Avian carcinoma virus.  
 OC Viruses; Retroviridae; Alpharetrovirus.  
 CX NCBI\_TaxID=11958;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85033920; PubMed=6092695;  
 RA Surraive P., Jansen H.W., Bister K., Rapp U.R.;  
 RT "3'-terminal region of avian carcinoma virus MH2 shares sequence  
 elements with avian sarcoma viruses Y73 and SR-A."  
 RL J. Virol. 52:703-705(1984).  
 DR EMBL; K03100; AAA42388.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 12 AA; 1466 MW; 72E4B884F30736DB CRC64;

Query Match 30.5%; Score 18; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNL 11  
 Db 2 HNL 4

## RESULT 13

Q28742 ID Q28742 PRELIMINARY; PRT; 7 AA.  
 AC Q28742; RT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Alpha-myosin heavy chain (Fragment).  
 OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 CX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84221901; PubMed=6328491;  
 RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,  
 RA Rabinowitz M.;  
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-  
 ventricular myosin heavy chains."  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).  
 DR EMBL; K01698; AAA31415.1; -.  
 DR PIR; I46868; I46868.  
 FT NON TER 1  
 SQ SEQUENCE 7 AA; 916 MW; 6B1B1A1E69326B0 CRC64;

Query Match 28.8%; Score 17; DB 6; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 OLMMN 10  
 Db 1 QXMD 5

## RESULT 14

Q15891 ID Q15891 PRELIMINARY; PRT; 9 AA.  
 AC Q15891; RT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE (Clone XP2E8B) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Placenta;  
 RA Lee C.-C., Yandani A., Wenhert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.I., Chnault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome-specific genes by reciprocal probing of  
 RT arrayed cDNAs and cosmid libraries."  
 RL Hum. Mol. Genet. 0:0-0(1995).  
 DR EMBL; L32131; AAA73881.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 1030 MW; B56635A1A33686D1 CRC64;

Query Match 28.8%; Score 17; DB 4; Length 9;  
 Best Local Similarity 44.4%; Pred. No. 1e+06;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 EIOGMN 12  
 Db 1 EIOGMN 9

## RESULT 15

Q9GD12 ID Q9GD12 PRELIMINARY; PRT; 9 AA.  
 AC Q9GD12; RT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Ribosomal protein S16 (Fragment).  
 GN RPS16.  
 OS Linospadix monostachya.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecaceae;

OC Areceae; Liospadicinae; Liospadix.  
OX NCBI\_taxid=131282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RA Aemussen C.B.; Chase M.W.;  
RT "Coding and noncoding plastid DNA in palm systematics";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; A0404941; CAC17917.1; -;  
DR GO; GO:0009507; C:Chloroplast; IEA.  
KW Chloroplast.  
FT NON TER 1 1  
FT NON TER 9 9  
SQ SEQUENCE 9 AA; 1106 MW; 1B9236C2C0441B50 CRC64;

Query Match 28.8%; Score 17; DB 8; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1e-06;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IOLM 8  
Db 6 VOLM 9

Search completed: May 18, 2004, 10:04:48  
Job time : 31.25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:42:39 ; Search time 45.75 Seconds  
(without alignments)  
74.111 Million cell updates/sec

Title: US-09-730-174A-5  
Perfect score: 59  
Sequence: 1 ANSEIQLMNMG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	89.8	11	3	AAY96968 Parathyro
2	50	84.7	11	6	ABG72607 Parathyro
3	50	84.7	12	6	ABG72608 Parathyro
4	45	78.0	10	2	AAB91644
5	45	78.0	10	3	AAY68767
6	45	78.0	10	4	AAB86219
7	45	78.0	10	6	ABR44166
8	45	76.3	9	4	AAB86225
9	43.5	73.7	11	2	AAY50600
10	43	72.9	9	3	AAB01862
11	43	72.9	9	3	AAY96966
12	40	67.8	9	2	AAB91645
13	40	67.8	9	3	AAB01863
14	40	67.8	9	3	AAY96961
15	40	67.8	9	4	AAB86220
16	40	67.8	10	4	AAB86932
17	40	67.8	11	4	AAB96931
18	40	67.8	11	4	AAB96931
19	40	67.8	11	4	AAB84770
20	40	67.8	12	4	AAB86914
21	40	67.8	12	4	AAB94769
22	38	64.4	12	2	AAB94765
23	35	59.3	10	6	ABP71484
24	35	59.3	11	1	AAB82547
25	35	59.3	11	4	AAB96892

26	35	59.3	11	6	ABP71485
27	35	59.3	11	6	ABP71483
28	35	59.3	12	4	AAB96891
29	35	59.3	12	6	ABP71482
30	33	55.9	9	3	AAB01864
31	33	55.9	9	3	AAY78849
32	33	55.9	9	3	AAY97062
33	32	54.2	8	2	AAR91646
34	32	54.2	8	3	AAB07467
35	32	54.2	8	4	AAB86221
36	30	50.8	9	3	AAB01866
37	27	45.8	7	2	AAR91647
38	27	45.8	7	4	AAB86222
39	27	45.8	10	5	ABG98580
40	27	45.8	10	5	ABG98582
41	27	45.8	10	5	ABG98581
42	27	45.8	11	4	ABU54029
43	27	45.8	12	2	AAR99301
44	27	45.8	12	2	AAB64520
45	27	45.8	12	3	AAB21270

## ALIGNMENTS

RESULT 1  
ID AAY96968 standard; peptide; 11 AA.  
XX  
AC AAY96968;  
XX  
DT 31-OCT-2000 (first entry)  
DE Parathyroid hormone N-terminal signaling domain (residues 1-11).  
XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
KW bone reformation; resorption; remodeling; tether; osteoporosis.  
XX  
OS Homo sapiens.  
XX  
FN WO200039278-A2.  
XX  
PD 06-JUL-2000.  
XX  
PF 30-DEC-1999; 99WO-US031108.  
XX  
PR 31-DEC-1998; 98US-0114577P.  
XX  
XX (GARD/) GARDELLA T J.  
XX (KRON/) KRONENBERG H M.  
XX (POTT/) POTTS J T.  
XX (JUEP/) JUEPPNER H.  
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX WPI; 2000-452384/39.  
XX  
PS Claim 4; Page 92; 119PP; English.  
XX  
CC Compounds of the structure or formula S-(L)-n-B, R1-S-(L)-n-R or S-(L)-n-R, are new. S is an amino terminal signaling functional domain of Parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased rethari activity, increasing cAMP

CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
CC regular injections to treat osteoporosis  
XX  
SQ Sequence 11 AA;  
Query Match 89.8%; Score 53; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0034;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 AVSEIQLMHNL 11  
1 AVSEIQLMHNL 11  
Db 1 AVSEIQLMHNL 11  
RESULT 2  
ABG72607  
ID ABG72607 standard; peptide; 11 AA.  
XX  
AC ABG72607;  
XX  
DT 11-FEB-2003 (first entry)  
XX  
DE Parathyroid hormone antigenic peptide 2-12.  
XX  
KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;  
KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.  
XX  
OS Homo sapiens.  
OS Mus sp.  
OS Rattus sp.  
OS Bos taurus.  
OS Sus scrofa.  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 6 /label= Leu, Phe  
FT  
FT  
XX  
EN US2002110871-A1.  
XX  
XX 15-AUG-2002.  
XX  
PD 05-DEC-2000; 2000US-00730174.  
XX  
PF 05-DEC-2000; 2000US-00730174.  
XX  
PR 05-DEC-2000; 2000US-00730174.  
XX  
XX (ZAHK/) ZAHRADNIK R J.  
PA (LAVI/) LAVIGNE J R.  
XX  
PI Zahradnik RJ, Lavigne JR;  
XX  
DR WPI; 2003-066685/06.  
XX  
XX New parathyroid hormone (PTH) antigenic peptide inducing the formation  
PT and isolation of antibodies having an affinity to it; useful for  
PT determining bioactive PTH levels in serum, plasma and/or cell culture  
PT media.  
XX  
XX Claim 1; Page 5; 11pp; English.  
XX  
CC The invention relates to a new antigenic peptide for inducing the  
CC formation and isolation of antibodies having an affinity to it; being  
CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
CC are; (1) a method for producing antibodies useful in the determination of  
CC PTH levels in a biological sample comprising: (a) providing at least one  
CC first peptide antigen comprising a peptide fragment of PTH; (b)  
CC administering the first peptide antigen to a host animal to induce  
CC antibody production; (c) monitoring the antibody titre produced; (d)  
CC isolating antisera produced in the host animal; and (e) selecting  
CC antisera from the isolated antisera produced in the host that is capable  
CC of binding to a second peptide antigen; (2) an antibody (ab) produced by

CC the method; and (3) test kits and analytical procedures used for the  
CC determination of bioactive intact PTH utilising (ab). The methods and  
CC compositions of the present invention are useful for determining  
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
CC  
CC The antigens, antibodies and methods of the present invention, as  
CC compared to prior art, have the particular advantages of possessing  
CC greater affinity for PTH, and in particular, are designed to have a novel  
CC recognition for amino acid residues extending beyond the first N-terminal  
CC PTH residue, and further have negligible cross-reactivity with the large  
CC non-molecular forms of PTH. PTH levels are an important parameter in  
CC patients suffering from hypercalcaemia, osteoporosis and primary  
CC hyperparathyroidism. The present sequence represents a PTH antigenic  
CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,  
CC canine and bovine PTH  
XX  
SQ Sequence 11 AA;  
Query Match 84.7%; Score 50; DB 6; Length 11;  
Best Local Similarity 90.9%; Pred. No. 0.012; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1;  
OY 2 VSEIQLMHNLG 12  
1 VSEIQLMHNLG 11  
Db 1 VSEIQLMHNLG 11  
RESULT 3  
ABG72608  
ID ABG72608 standard; peptide; 12 AA.  
XX  
AC ABG72608;  
XX  
DT 11-FEB-2003 (first entry)  
XX  
DE Parathyroid hormone antigenic peptide 1-12.  
XX  
KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;  
KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.  
XX  
XX  
OS Homo sapiens.  
OS Mus sp.  
OS Rattus sp.  
OS Bos taurus.  
OS Sus scrofa.  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /label= Ser, Ala  
FT Misc-difference 7 /label= Leu, Phe  
FT  
FT  
XX  
EN US2002110871-A1.  
XX  
XX 15-AUG-2002.  
XX  
PD 05-DEC-2000; 2000US-00730174.  
XX  
PF 05-DEC-2000; 2000US-00730174.  
XX  
PR 05-DEC-2000; 2000US-00730174.  
XX  
XX (ZAHK/) ZAHRADNIK R J.  
PA (LAVI/) LAVIGNE J R.  
XX  
PI Zahradnik RJ, Lavigne JR;  
XX  
DR WPI; 2003-066685/06.  
XX  
XX New parathyroid hormone (PTH) antigenic peptide inducing the formation  
PT and isolation of antibodies having an affinity to it; useful for  
PT determining bioactive PTH levels in serum, plasma and/or cell culture  
PT media.  
XX  
XX Claim 2; Page 5; 11pp; English.

XX The invention relates to a new antigenic peptide for inducing the  
 CC formation and isolation of antibodies having an affinity to it, being  
 CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
 CC are, (1) a method for producing antibodies useful in the determination of  
 CC PTH levels in a biological sample comprising: (a) providing at least one  
 CC first peptide antigen comprising a peptide fragment of PTH; (b)  
 CC administering the first peptide antigen to a host animal to induce  
 CC antibody production; (c) monitoring the antibody titre selecting (d)  
 CC isolating antisera produced in the host animal, and (e) selecting  
 CC antisera from the isolated antisera produced in the host that is capable  
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by  
 CC the method; and (3) test kits and analytical procedures used for the  
 CC determination of bioactive intact PTH utilising (ab). The methods and  
 CC compositions of the present invention are useful for determining  
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
 CC The antigens, antibodies and methods of the present invention, as  
 CC compared to prior art, have the particular advantages of possessing  
 CC greater affinity for PTH, and in particular, are designed to have a novel  
 CC recognition for amino acid residues extending beyond the first N-terminal  
 CC PTH residue, and further have negligible cross-reactivity with the large  
 CC non-molecular forms of PTH. PTH levels are an important parameter in  
 CC patients suffering from hypercalcaemia, osteoporosis and primary  
 CC hyperparathyroidism. The present sequence represents a PTH antigenic  
 CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,  
 CC canine and bovine PTH  
 CC  
 SQ Sequence 12 AA;  
 Query Match 84.7%; Score 50; DB 6; Length 12;  
 Best Local Similarity 90.9%; Pred. No. 0.014;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VSSEIQMLNNG 12  
 Db 2 VSSEIQMLNNG 12  
 RESULT 4  
 AAR91644  
 ID AAR91644 standard; peptide; 10 AA.  
 AC AAR91644;  
 XX  
 XX 06-NOV-1996 (first entry)  
 DT  
 XX  
 DE Human parathyroid hormone antigenic peptide hPTH 1-10.  
 XX  
 KM Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
 KM diagnosis; active hPTH 1-37.  
 XX  
 OS Synthetic.  
 XX  
 PN DE4434551-A1.  
 XX  
 PD 04-APR-1996.  
 XX  
 PF 28-SEP-1994; 94DE-04434551.  
 XX  
 PR 28-SEP-1994; 94DE-04434551.  
 PA (FORS/) FORSSMANN W.  
 XX  
 PI Adermann K, Forsmann W, Hock D, Maegerlein M;  
 XX  
 DR WP1; 1996-180391/19.  
 PT New antigenic peptide(s) from human parathyroid hormone - and antibodies  
 PT generated using them, able to distinguish between active and inactive  
 PT forms of the hormone.  
 PS Claim 2; Page 4; 5pp; German.  
 XX

CC The present sequence is a specific example of claimed immunogenic  
 CC peptides having a sequence from hPTH(1-37) which includes the N- or C-  
 CC terminal alpha-helical region and/or the non-structured region of the  
 CC hormone. Antibodies and their binding fragments generated by injecting an  
 CC animal with the peptides are useful as diagnostic reagents for  
 CC determination of biologically active hPTH(1-37)  
 CC  
 SQ Sequence 10 AA;  
 Query Match 78.0%; Score 46; DB 2; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 0.061;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AVSEIQMLNHN 10  
 Db 1 AVSEIQMLNHN 10  
 RESULT 5  
 AAY68767  
 ID AAY68767 standard; peptide; 10 AA.  
 XX  
 AC AAY68767;  
 XX  
 DT 05-MAY-2000 (first entry)  
 DE  
 XX Amino acids 1-10 of a parathyroid hormone (PTH).  
 XX  
 KM Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;  
 KM slimming treatment; cellulite; skin firming.  
 OS Unidentified.  
 XX  
 PN WO200004047-A1.  
 XX  
 PD 27-JAN-2000.  
 XX  
 PF 07-JUL-1999; 99MO-FR001687.  
 XX  
 PR 17-JUL-1998; 98FR-00009193.  
 XX  
 PA (SEDE-) SEDERMA.  
 XX  
 PI Lintner K;  
 XX  
 DR WP1; 2000-171243/15.  
 XX  
 DE New parathyroid hormone fragment peptides, used as lipolysis stimulants  
 PT in topically applied cosmetic compositions for slimming treatment of  
 PT excessive weight in hips and thighs.  
 XX  
 PS Claim 1; Page 8; 18pp; French.  
 XX  
 CC The present sequence represents a parathyroid hormone (PTH) fragment,  
 CC comprising amino acids 1-10. Parathyroid hormone fragments of the  
 CC invention have lipolytic stimulating activity (especially when topically  
 CC administered). The lipolytic activity of the peptides is enhanced when  
 CC they are chemically modified to increase their lipophilicity. The  
 CC peptides are used in cosmetic or dermatological compositions for skin  
 CC care. They are especially used for slimming treatment of excessive weight  
 CC in the thighs and hips, in the treatment of cellulite and for skin  
 CC firming  
 CC  
 SQ Sequence 10 AA;  
 Query Match 78.0%; Score 46; DB 3; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 0.061;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AVSEIQMLNHN 10  
 Db 1 VSSEIQMLNHN 10



```

RESULT 6
ID AAB86219 standard; peptide; 10 AA.
XX
AC AAB86219;
XX
DE 03-SEP-2001 (first entry)
XX
DE Human parathyroid hormone immunogenic peptide SEQ ID 1.
XX
KM Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
XX diagnoses; calcium-metabolism disorder; osteopathy; antagonist;
XX hypo-parathyroidism; hyper-parathyroidism.
XX
OS Homo sapiens.
XX
PN DE1996:350-A1.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99DE-01061350.
XX
PR 17-DEC-1999; 99DE-01061350.
XX
PA (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI Ambruuster FP;
XX
DR WPI; 2001-376318/40.
XX
PT Determining the content of physiologically active parathyroid hormone,
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT reactive with different epitopes.
XX
PS Disclosure; Page 3; 10pp; German.
XX
XX This invention describes a novel method for determining (M1) the content
XX of active parathyroid hormone (A) by treating a sample with (i) antibody
XX (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
XX and including the N-terminal residue and (ii) antibody (Ab2) that
XX recognizes an epitope within the receptor-binding site of (A). The number
XX of molecules that react with both antibodies is determined and used to
XX calculate the content of physiologically active (A). The method is used
XX for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
XX hyper-parathyroidism. The method (unlike known assays) recognizes that
XX (i) some fragments of (A) shorter than the complete (84 aa) peptide are
XX active, and (ii) that apparently intact peptide may be biologically
XX inactive, and also takes into account the fact that some fragments of (A)
XX are antagonistic (these have the receptor-binding site but lack the N-
XX terminus). It thus provides a true measure of the content of
XX physiologically active (A); contrast methods that measure intact peptide
XX and its 1-37 fragment which may produce falsely high values. This
XX sequence represents a peptide fragment used to illustrate the method of
XX the invention
XX
SQ Sequence 10 AA;
XX
Query Match 78.0%; Score 46; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.061;
Matches 9; Conservative 1; Mismatches 0; Gaps 0
QY 1 ANSEIQLMEN 10
:|||||||
DB 1 SVSEIQLMEN 10

```

DT	04-AUG-2003	(first entry)	
XX			
XX			
DE	Human parathyroid hormone (hPTH) fragment (residues 1-10).		
XX			
KM	Fusion peptide, cat: hPTHDP; parathyroid hormone; skin, cosmetic;		
XX	lipolysis; human; hPTH.		
XX			
OS	Homo sapiens.		
XX			
FN	WO2003035697-A1.		
PD	01-MAY-2003.		
XX			
PF	06-MAY-2002; 2002WO-KR000835.		
XX			
PR	27-SEP-2001; 2001KR-00060245.		
XX	15-MAR-2002; 2002KR-00014062.		
XX			
PA	(GLDS ) LG HOUSEHOLD & HEALTH CARE LTD.		
PI	Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H;		
PI	Chang M;		
XX			
DR	WPI; 2003-468288/44.		
XX			
PS	Claim 5; Page 6; 32pp; English.		
XX			
CC	The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-		
CC	penetrating Tat peptide is bound to human parathyroid hormone-derived		
CC	peptide (hPTHDP). The fusion peptide is useful as a component of skin		
CC	stimulating cosmetic composition. The fusion peptide does not cause		
CC	irritation, easily and safely penetrates into integument and endothelium,		
CC	does not cause skin disease and has superior lipolysis effects, and is		
CC	durable. The present sequence represents a human parathyroid hormone		
CC	(hPTH) fragment that can be used to construct the fusion peptide		
XX			
SQ	Sequence 10 AA;		
Query Match		78.0%; Score 46; DB 6; Length 10;	
Best Local Similarity	90.0%;	Pred. No. 0.061;	
Matches	9; Conservative	1; Mismatches	0; Indels 0; Gaps 0.
QY	1 AVSEIQLMN 10		
DB	1 SVSEIQLMN 10		
RESULT 8			
AAB86225			
ID	AAB86225 standard; peptide; 9 AA.		
XX			
AC	AAB86225;		
XX			
DT	03-SEP-2001 (first entry)		
XX			
DE	Human parathyroid hormone immunogenic peptide. SEQ ID 7.		
XX			
KM	Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;		
KW	diagnosis; calcium-metabolism disorder; osteopathy; antagonist;		
KW	hypo-parathyroidism; hyper-parathyroidism.		
XX			
OS	Homo sapiens.		
XX			
FN	DE1961350-A1.		
XX			
PD	21-JUN-2001.		
XX			
PF	17-DEC-1999; 99DE-01061350.		
XX			

PR 17-DEC-1999; 99DE-01061350.  
 XX (IMMU-) IMMUNDIAGNOSTIK AG.  
 XX Armbruster FP;  
 PI WPI; 2001-376318/40.  
 DR WPI; 2001-376318/40.  
 XX  
 PT Determining the content of physiologically active parathyroid hormone,  
 PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
 PT reactive with different epitopes.  
 PS  
 PS Disclosure; Page 3; 10pp; German.  
 CC This invention describes a novel method for determining (M1) the content  
 CC of active parathyroid hormone (A) by treating a sample with (i) antibody  
 CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
 CC and including the N-terminal residue and (ii) antibody (Ab2) that  
 CC recognizes an epitope within the receptor-binding site of (A). The number  
 CC of molecules that react with both antibodies is determined and used to  
 CC calculate the content of physiologically active (A). The method is used  
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
 CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
 CC active and (ii) that apparently intact peptide may be biologically  
 CC inactive, and also takes into account the fact that some fragments of (A)  
 CC are antagonistic (these have the receptor-binding site but lack the N-  
 CC terminus). It thus provides a true measure of the content of  
 CC physiologically active (A); contrast methods that measure intact peptide  
 CC and its 1-37 fragment which may produce falsely high values. This  
 CC sequence represents a peptide fragment used to illustrate the method of  
 CC the invention  
 CC  
 XX Sequence 9 AA;  
 SQ  
 Query Match 76.3%; Score 45; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VSEIQLMEN 10  
 DB 1 VSEIQLMEN 9  
 RESULT 9  
 AAY50600  
 ID AAY50600 standard; peptide; 11 AA.  
 XX  
 AC AAY50600;  
 XX  
 XX 09-FEB-2000 (first entry)  
 XX  
 XX Resin bound cyclic peptide 33.  
 XX  
 DE Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;  
 XX hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;  
 XX osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;  
 KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.  
 KW  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH MISC-difference 1  
 FT MISC-difference 1 /note= "FMOC-Ala"  
 FT MISC-difference 3 /note= "Ser(OtBu)"  
 FT MISC-difference 4 /note= "Glu(OtBu)"  
 FT MISC-difference 6 /note= "Glu(OtBu)"  
 FT MISC-difference 9 /note= "Gln(Trt)"  
 FT MISC-difference 9 /note= "His(Trt)"  
 FT MISC-difference 10

FT /note= "Asn(Trt)"  
 XX  
 XX WO9952933-A1.  
 XX  
 XX 21-OCT-1999.  
 PD  
 XX 15-APR-1999; 99WO-US008435.  
 XX  
 XX 15-APR-1999; 98US-0081897P.  
 XX  
 XX (RHON) RHONE-POULENC RORER PHARM INC.  
 PA  
 XX  
 PI Sledeski AM, Mancel JJ;  
 PS  
 PS WPI; 1999-633822/54.  
 DR  
 XX  
 XX Convergent synthesis of peptides for treating e.g. bone disorders.  
 PT  
 PT Disclosure; Page 75; 85pp; English.  
 PS  
 XX This invention describes a novel method for the preparation of peptides  
 CC (ii) that contain both cyclic and linear peptide fragments comprises  
 CC sequential reaction of a resin-bound linear fragment with the cyclic  
 CC fragment in N-protected form and optionally other linear fragments. The  
 CC products of the invention have osteopathic and hypotensive activity. (ii)  
 CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The  
 CC method is particularly used to prepare cyclic peptide analogs of  
 CC parathyroid hormone (PTH) or PTH-related peptides which are useful for  
 CC treating diseases that respond to treatment with agents that bind to PTH  
 CC receptors (with or without activation of adenylate cyclase activity), e.g.  
 CC hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-  
 CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also  
 CC for promoting repair of bone fractures. Separate synthesis of the cyclic  
 CC fragment allows convergent synthesis of resin-bound (ii), with better  
 CC yields and higher throughput. The difficulties associated with  
 CC preparation of the bridged fragment are confined to a small peptide which  
 CC can be purified before reaction with the resin-bound component. AAY5060-  
 CC Y50614 represent the peptide fragments described in the method of the  
 CC invention  
 CC  
 XX Sequence 11 AA;  
 SQ  
 Query Match 73.7%; Score 43.5; DB 2; Length 11;  
 Best Local Similarity 91.7%; Pred. No. 0.2;  
 Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 AVSEIQLMHNG 12  
 DB 1 AVSEIQ-LHNG 11  
 RESULT 10  
 AAB01862  
 ID AAB01862 standard; peptide; 9 AA.  
 XX  
 AC AAB01862;  
 XX  
 XX 11-SEP-2000 (first entry)  
 XX  
 DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.  
 XX  
 XX Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;  
 KW calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;  
 KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO2000023594-A1.  
 XX  
 XX 27-APR-2000.  
 PD  
 XX 20-OCT-1999; 99WO-US024481.  
 XX

XX	PR	22-OCT-1998;	98US-0105530P.
XX	PA	(GARD/) GARDELLA T J.	
XX	PA	(KRON/) KRONENBERG H M.	
XX	PT	(POT/) POTTS J T.	
XX	PA	(JUEP/) JUEPPNER H.	
PI	FI	Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;	
XX	DR	WPI; 2000-339693/29.	
XX	PT	Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic acids that encode them, useful for treating osteoporosis.	
XX	PS	Disclosure; Page 26; 73pp; English.	
XX	CC	The invention relates to a novel parathyroid hormone (PTH) peptide (AA01859) and parathyroid hormone-related peptide (PTHrP; AA01860), and biologically active derivatives thereof (AA01857-B01858, AA01861-B01863). The peptides of the invention are at least 85% identical to the generic peptide of the formula: X1-Val-ser-Glu-X2-Gln-Ileu-X3-His-X4-X5-Gly-Lys-X6 (AA01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser; provided that the peptide is not PTHrP(1-14). The peptides of the invention also encompass fragments of peptides of the invention consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-terminal derivatives. PTH is a major regulator of calcium homeostasis, and is necessary for the normal function of the gastrointestinal, skeletal, neurological system, neuromuscular and cardiovascular systems. It binds to both PTH-1 receptors on osteoblasts and renal tubular cells, and to the recently identified PTH-2 receptor. PTH has a potent anabolic effect on the skeleton, and mediates calcium reabsorption, enhances phosphate clearance and vitamin D synthesis in the kidney. A homologous class of protein hormones, the PTH-related proteins (PTHrP) mimic some of the renal and skeletal actions of PTH, and also bind to the PTH-1 receptor. They do not bind to the PTH-2 receptor. The peptides of the invention are either agonists of PTH-1 and PTH-2 receptors (AA01858, AA01861-P01866) or are PTH-1/PTH-2 receptor antagonists (AA01867-B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of conditions characterised by a decrease in bone mass, such as osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating medical disorders that arise from excessive or altered action of the PTH-1/PTH-2 receptor. Detectably labelled peptides of the invention are also useful in the determination of rates of bone formation, bone resorption and/or bone remodelling in a patient. The peptides of the invention are "unimised" versions of PTH or PTHrP which are inexpensive to prepare by conventional synthetic chemistry, and can be delivered to a patient via non-parenteral routes. Sequences AA01858 and AA01861-B01866 represent PTH-1/PTH-2 receptor agonists	
CC	CC	Sequence 9 AA:	
SQ	XX		
		Query Match 72.9%; Score 43; DB 3; Length 9;	
		Best Local Similarity 100.0%; Pred. No. 1.4e+06;	
		Matches 9; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;	
OY	I	AVSEIQLMH 9	
Dd	1	AVSEIQLMH 9	
RESULT 11			
ID	AAV96966	standard; peptide; 9 AA.	
AC	AAV96966		
DT	31-OCT-2000	(first entry)	
DE	Parathyroid hormone N-terminal signaling domain (residues 1-9).		
KX	PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;		

```

XX bone reformation; resorption; remodeling; tether; osteoporosis.
XX Homo sapiens.
XX PN WO200039278-A2.
XX PD 06-JUL-2000.
XX PF 30-DEC-1999; 59WO-US031108.
XX PR 31-DEC-1998; 98US-0114577P.
XX PA (GARD/) GARDELLA T J.
XX PA (KRON/) KRONENBERG H M.
XX PA (POT/) POTTS J T.
XX PA (JUEP/) JUEPPNER H.
XX PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX DR
XX PT New compound comprising an amino terminal signaling functional domain
XX PT linked to a carboxy-terminal binding portion of parathyroid hormone for
XX PT treating mammalian conditions characterized by decreases in bone mass.
XX
XX PS Claim 4; Page 92; 119p; English.
XX
XX CC Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or S-(L) n
XX CC -R, are new. S is an amino terminal signaling functional domain of
XX CC parathyroid hormone (PTH). L is a linker molecule present n times, (where
XX CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
XX CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the
XX CC PTH-1 receptor signal sequence; and R is a portion of) PTH-1 receptor
XX CC sequence. The new compounds are used for treating mammalian conditions
XX CC characterized by decreases in bone mass, determining rates of bone
XX CC reformation, bone resorption and/or bone remodeling, treating diseases
XX CC and disorders associated with decreased tether activity, increasing BMP
XX CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
XX CC non-peptide PTH (claimed). The new compound can be administered by
XX CC inhalation unlike the large native PTH or PTHrp which avoids the need for
XX CC regular injections to treat osteoporosis
XX
SQ Sequence 9 AA:

Query Match 72.9%; Score 43; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1,4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 AVSEIQLMH 9
   |||||
Db 1 AVSEIQLMH 9

RESULT 12
AAR91645
ID AAR91645 standard; peptide; 9 AA.
XX
XX AAR91645;
XX AC
XX DT 06-NOV-1996 (first entry)
XX DE Human parathyroid hormone antigenic peptide hPTH 1-9.
XX KM Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
XX KM diagnosis; active hPTH 1-37.
XX OS Synthetic.
XX PN DE4434551-A1.
XX PD 04-APR-1996.
XX PF 28-SEP-1994; 94DE-04434551.

```

XX	28-SEP-1994;	94DE-04434551.	
FR	(FORS/)	FORSSMANN W.	
PA	Adermann K,	Forsmann W,	Hock D, Maegerlein M;
XX	WI;	1996-180391/19.	
DR			
XX			
PT	New antitonic peptide(s)	from human parathyroid hormone - and antibodies	
PT	generated using them,	able to distinguish between active and inactive	
PT	forms of the hormone.		
XX			
PS	Claim 2;	Page 4;	5pp; German.
XX			
CC	The present sequence is a specific example of claimed immunogenic		
CC	peptides having a sequence from hPTH(1-37) which includes the N- or C-		
CC	terminal alpha-helical region and/or the non-structured region of the		
CC	hormone. Antibodies and their binding fragments generated by injecting an		
CC	animal with the peptides are useful as diagnostic reagents for		
CC	determination of biologically active hPTH(1-37)		
XX			
SQ	Sequence 9 AA;		
XX			
Query Match	67.8%;	Score 40;	DB 2; Length 9;
Best Local Similarity	88.9%;	Pred. No. 1.4e+06;	
Matches	8;	Conservative 1;	Mismatches 0;
		Indels 0;	Gaps 0
Cy	1 AVSEIQLMH 9		
	:		
Db	1 SVSEIQLMH 9		
XX			
RESULT 13			
AB01863			
ID	AB01863	standard;	peptide; 9 AA.
XX			
AC	AA01863;		
XX			
DT	11-SEP-2000	(first entry)	
XX			
DE	PTH(1-14)/PTHrP(1-14)-derived peptide.	SEQ ID NO:7.	
XX			
KW	Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;		
KW	calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;		
KW	bone synthesis; agonist; osteoporosis; non-parenteral delivery.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PN	WO200023594-A1.		
XX			
PD	27-APR-2000.		
XX			
PF	20-OCT-1999;	99MO-US024481.	
XX			
PR	22-OCT-1998;	98US-0105530P.	
XX			
PA	(GARD/)	GARDELLA T J.	
PA	(KRON/)	KRONENBERG H M.	
PA	(POTT/)	POTTS J T.	
PA	(JUEP/)	JUEPNER H.	
XX			
PI	Gardella TJ,	Kronenberg HM,	Potts JT, Juepner H;
XX			
DR	WI;	2000-339693/29.	
XX			
PT	Parathyroid hormone (PTH) peptides;	PTH related peptides and the nucleic	
PT	acids that encode them;	useful for treating osteoporosis.	
XX			
XX	Disclosure;	Page 26;	73pp; English.
XX			
CC	The invention relates to a novel parathyroid hormone (PTH) peptide		

(AAB01869) and parathyroid hormone-related peptide (PTHrP; AAB01860), and biologically active derivatives thereof (AAB01867-B01869, AAB01861-CC B01869). The peptides of the invention are at least 85% identical to the generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-Gly-Lys-X6 (AAB01867) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser; provided that the peptide is not PTHrP(1-14). The peptides of the invention also encompass fragments of peptides of the invention consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-terminal derivatives. PTH is a major regulator of calcium homeostasis, and is necessary for the normal function of the gastrointestinal, skeletal, neurological system, neuromuscular and cardiovascular systems. It binds to both PTH-1 receptors on osteoblasts and renal tubular cells, and to the recently identified PTH-2 receptor. PTH has a potent anabolic effect on the skeleton, and mediates calcium reabsorption, enhances phosphate clearance and vitamin D synthesis in the kidney. A homologous class of protein hormones, the PTH-related proteins (PTHrP) mimic some of the renal and skeletal actions of PTH, and also bind to the PTH-1 receptor. They do not bind to the PTH-2 receptor. The peptides of the invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858, AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of conditions characterized by a decrease in bone mass, such as osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating medical disorders that arise from excessive or altered action of the PTH-1/PTH-2 receptor. Detectably labelled peptides of the invention are also useful in the determination of rates of bone formation, bone resorption and/or bone remodelling in a patient. The peptides of the invention are "minimised" versions of PTH or PTHrP, which are inexpensive to prepare by conventional synthetic chemistry, and can be delivered to a patient via non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent PTH-1/PTH-2 receptor agonists

SQ Sequence 9 AA:

Query Match 67.8%; Score 40; DB 3; Length 9;  
Best Local Similarity 80.9%; Pred. No. 1,4e+06;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AVSEIQLMH 9  
||| ||| :  
(KRONENBERG H M,  
DB 1 AVSEIQLLH 9

RESULT 14  
AA9Y6981  
AA9Y6981 standard; peptide; 9 AA.

AC AA9Y6981;  
XX  
DT 31-OCT-2000 (first entry)  
XX  
DE Parathyroid hormone N-terminal signaling domain.  
XX  
KM PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
XX bone reformation; resorption; remodeling; tether1; osteoporosis.  
XX  
OS Homo sapiens.  
XX  
PM WO200039278-A2.  
XX  
PD 06-JUL-2000.  
XX  
PF 30-DEC-1999; 99WO-USO31108.  
XX  
PR 31-DEC-1998; 98US-0114577P.  
XX  
PA (GARDELIA T J,  
XX (KRONENBERG H M,  
PA (POTTS J T,  
XX (JUEPPNER H,  
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H,

XX  
DR WPI; 2000-452364/39.  
XX  
PT New compound comprising an amino terminal signaling functional domain  
PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
PT treating mammalian conditions characterized by decreases in bone mass.  
XX  
PS Claim 11; Page 93; 119pp; English.  
XX  
CC Compounds of the structure or formula S-(L)-n-B, R1-S-(L)-n-R or S-(L)-n  
CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the  
CC PTH-1 receptor signal sequence; and R is a portion of PTH-1 receptor  
CC sequence. The new compounds are used for treating mammalian conditions  
CC characterized by decreases in bone mass, determining rates of bone  
CC reformation, bone resorption and/or bone remodeling, treating diseases  
CC and disorders associated with decreased bone activity, increasing bone  
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHrp which avoids the need for  
CC regular injections to treat osteoporosis  
XX  
SQ Sequence 9 AA;  
Query Match 67.8%; Score 40; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVSEIQLMH 9  
Db 1 SVSEIQLMH 9  
RESULT 15  
AAB86220  
ID AAB86220 standard; peptide; 9 AA.  
XX  
AC AAB86220;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE Human parathyroid hormone immunogenic peptide SEQ ID 2.  
XX  
KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
KW hypo-parathyroidism; hyper-parathyroidism.  
XX  
OS Homo sapiens.  
XX  
PN DE19961350-A1.  
XX  
PD 21-JUN-2001.  
XX  
PF 17-DEC-1999; 99DE-01061350.  
XX  
PR 17-DEC-1999; 99DE-01061350.  
XX  
PA (IMMU-) IMMUNDIAGNOSTIK AG.  
XX  
PI Armbruster FP;  
XX  
DR WPI; 2001-376318/40.  
XX  
PT Determining the content of physiologically active parathyroid hormone,  
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
PT reactive with different epitopes.  
XX  
PS Disclosure; Page 3; 10pp; German.  
XX  
CC This invention describes a novel method for determining (M1) the content  
CC of active parathyroid hormone (A) by treating a sample with (1) antibody

CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
CC and including the N-terminal residue and (ii) antibody (Ab2) that  
CC recognizes an epitope within the receptor-binding site of (A). The number  
CC of molecules that react with both antibodies is determined and used to  
CC calculate the content of physiologically active (A). The method is used  
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
CC active and (ii) that apparently intact peptide may be biologically  
CC inactive, and also takes into account the fact that some fragments of (A)  
CC are antagonistic (these have the receptor-binding site but lack the N-  
CC terminus). It thus provides a true measure of the content of  
CC physiologically active (A); contrast methods that measure intact peptide  
CC and its 1-37 fragment which may produce falsely high values. This  
CC sequence represents a peptide fragment used to illustrate the method of  
CC the invention  
XX  
SQ Sequence 9 AA;  
Query Match 67.8%; Score 40; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVSEIQLMH 9  
Db 1 SVSEIQLMH 9  
Search completed: May 18, 2004, 10:01:54  
Job time : 45.75 secs

Tue May 18 12:03:07 2004

us-09-730-174a-5.closed.rapb

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 10:04:51 ; Search time 33.25 Seconds

(without alignments)  
100.425 Million cell updates/sec

Title: US-09-730-174A-5

Perfect score: 59

Sequence: 1 AVSEIQMLHNLG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 166097

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	59	100.0	12	9	US-09-730-174A-5	Sequence 5, Appli
2	56	94.9	12	9	US-09-730-174A-3	Sequence 3, Appli
3	55	93.2	11	9	US-09-730-174A-1	Sequence 1, Appli
4	55	93.2	12	9	US-09-730-174A-6	Sequence 6, Appli
5	52	88.1	12	9	US-09-730-174A-4	Sequence 4, Appli
6	51	86.4	11	9	US-09-730-174A-2	Sequence 2, Appli
7	46	78.0	10	14	US-10-168-185-1	Sequence 1, Appli
8	45	76.3	9	14	US-10-168-185-7	Sequence 7, Appli
9	43	72.3	9	14	US-10-192-673-6	Sequence 6, Appli
10	41	69.5	8	14	US-10-168-185-8	Sequence 8, Appli
11	40	67.8	9	14	US-10-192-673-7	Sequence 7, Appli
12	40	67.8	9	14	US-10-168-185-2	Sequence 2, Appli
13	33	55.2	8	14	US-10-192-673-8	Sequence 8, Appli
14	32	54.2	8	14	US-10-168-185-3	Sequence 3, Appli
15	30	50.8	9	14	US-10-192-673-10	Sequence 10, Appli

16	28	47.5	12	14	US-10-319-130-16	Sequence 16, Appli
17	27	45.8	7	14	US-10-168-185-4	Sequence 4, Appli
18	26	44.1	10	14	US-10-033-741-61	Sequence 61, Appli
19	25	42.4	9	9	US-09-746-945-6	Sequence 6, Appli
20	25	42.4	11	12	US-09-747-287-185	Sequence 185, App
21	24	40.7	10	9	US-09-826-290-27	Sequence 27, Appli
22	24	40.7	10	16	US-10-264-309-369	Sequence 369, App
23	24	40.7	11	12	US-10-609-217-41	Sequence 41, Appli
24	24	40.7	11	12	US-10-632-388-41	Sequence 41, Appli
25	24	40.7	11	12	US-10-651-723-41	Sequence 41, Appli
26	24	40.7	11	12	US-10-645-723-41	Sequence 41, Appli
27	24	40.7	11	16	US-10-666-686-41	Sequence 41, Appli
28	24	40.7	11	16	US-10-653-048-41	Sequence 41, Appli
29	24	40.7	12	14	US-10-286-457-294	Sequence 294, App
30	23	39.0	6	14	US-10-168-185-5	Sequence 5, Appli
31	23	39.0	7	14	US-10-286-457-469	Sequence 469, App
32	23	39.0	7	15	US-10-368-280-12	Sequence 12, Appli
33	23	39.0	7	15	US-10-374-038-12	Sequence 12, Appli
34	23	39.0	9	9	US-09-894-018-332	Sequence 332, App
35	23	39.0	9	10	US-09-821-734-4	Sequence 4, Appli
36	23	39.0	9	10	US-09-854-248-11	Sequence 11, Appli
37	23	39.0	9	12	US-10-253-286-288	Sequence 288, App
38	23	39.0	9	14	US-10-094-699-50	Sequence 50, Appli
39	23	39.0	9	15	US-10-117-937-249	Sequence 249, App
40	23	39.0	9	15	US-10-117-937-249	Sequence 249, App
41	23	39.0	10	14	US-10-094-699-49	Sequence 49, Appli
42	23	39.0	10	14	US-10-232-187-8	Sequence 8, Appli
43	23	39.0	10	14	US-10-168-185-11	Sequence 11, Appli
44	23	39.0	10	15	US-10-026-066-31	Sequence 31, Appli
45	23	39.0	10	15	US-10-026-066-83	Sequence 83, Appli

#### ALIGNMENTS

RESULT 1  
US-09-730-174A-5  
Sequence 5, Application US/09730174A  
Patent No. US20020110871A1  
GENERAL INFORMATION:  
APPLICANT: Zatradihk, R.J.  
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
FILE REFERENCE: IMUNE-001A  
CURRENT APPLICATION NUMBER: US/09/730,174A  
CURRENT FILING DATE: 2000-12-05  
NUMBER OF SEQ ID NOS: 12  
SEQ ID NO 5  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
US-09-730-174A-5

Query Match 100.0%; Score 59; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQMLHNLG 12  
DB 1 AVSEIQMLHNLG 12

RESULT 2  
US-09-730-174A-3  
Sequence 3, Application US/09730174A  
Patent No. US20020110871A1  
GENERAL INFORMATION:  
APPLICANT: Zatradihk, R.J.  
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
FILE REFERENCE: IMUNE-001A  
CURRENT APPLICATION NUMBER: US/09/730,174A  
CURRENT FILING DATE: 2000-12-05  
NUMBER OF SEQ ID NOS: 12  
SEQ ID NO 5  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
US-09-730-174A-3

```

; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3
```

```

Query Match          94.8%; Score 56; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0022;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AVSEIQLMNHLG 12
       :|||||
Db      1 SVSEIQLMNHLG 12
```

```

RESULT 3
US-09-730-174A-1
; Sequence 1, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: INJUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1
```

```

Query Match          93.2%; Score 55; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VSEIQLMNHLG 12
       :|||||
Db      1 VSEIQLMNHLG 11
```

```

RESULT 4
US-09-730-174A-6
; Sequence 6, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: INJUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-6
```

```

Query Match          93.2%; Score 55; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      1 AVSEIQLMNHLG 12
       :|||||
Db      1 AVSEIQLMNHLG 12
```

```

RESULT 5
US-09-730-174A-4
; Sequence 4, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: INJUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4
```

```

Query Match          88.1%; Score 52; DB 9; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.011;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      1 AVSEIQLMNHLG 12
       :|||||
Db      1 SVSEIQLMNHLG 12
```

```

RESULT 6
US-09-730-174A-2
; Sequence 2, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: INJUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-2
```

```

Query Match          86.4%; Score 51; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      2 VSEIQLMNHLG 12
       :|||||
Db      1 VSEIQLMNHLG 11
```

```

RESULT 7
US-10-168-185-1
; Sequence 1, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Mischler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
```

;; TITLE OF INVENTION: Activity in a Human Sample  
;; FILE REFERENCE: HLZ-004US  
;; CURRENT APPLICATION NUMBER: US/10/168,185  
;; CURRENT FILING DATE: 2002-06-17  
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911  
;; PRIOR FILING DATE: 2000-12-18  
;; PRIOR APPLICATION NUMBER: DE 19961350  
;; PRIOR FILING DATE: 1999-12-17  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-168-185-1

Query Match 78.0%; Score 46; DB 14; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.11;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVESEIQLMHN 10  
DB 1 SVSEIQLMHN 10

RESULT 8  
US-10-168-185-7  
;; Sequence 7, Application US/10/168185  
;; Publication No. US20030175802A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Armbruster, Franz Paul  
;; APPLICANT: Missbichler, Albert  
;; APPLICANT: Schmidt-Gayk, Heinrich  
;; APPLICANT: Roth, Heinz-Jürgen  
;; TITLE OF INVENTION: Method for Determining Parathormone  
;; TITLE OF INVENTION: Activity in a Human Sample  
;; FILE REFERENCE: HLZ-004US  
;; CURRENT APPLICATION NUMBER: US/10/168,185  
;; CURRENT FILING DATE: 2002-06-17  
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911  
;; PRIOR FILING DATE: 2000-12-18  
;; PRIOR APPLICATION NUMBER: DE 19961350  
;; PRIOR FILING DATE: 1999-12-17  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 7  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-168-185-7

Query Match 76.3%; Score 45; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHN 10  
DB 1 VSEIQLMHN 9

RESULT 9  
US-10-192-673-6  
;; Sequence 6, Application US/10/192673  
;; Publication No. US20030166838A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gardella, Thomas J.  
;; APPLICANT: Kronenberg, Henry  
;; APPLICANT: Potts, John T.  
;; APPLICANT: Juppner, Harald  
;; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
;; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
;; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)  
;; FILE REFERENCE: 0609.4570002

;; CURRENT APPLICATION NUMBER: US/10/192,673  
;; CURRENT FILING DATE: 2002-07-11  
;; PRIOR APPLICATION NUMBER: U.S. 09/421,379  
;; PRIOR FILING DATE: 1999-10-20  
;; PRIOR APPLICATION NUMBER: U.S. 60/105,530  
;; PRIOR FILING DATE: 1998-10-22  
;; NUMBER OF SEQ ID NOS: 13  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 6  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-192-673-6

Query Match 72.9%; Score 43; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVESEIQLMH 9  
DB 1 AVESEIQLMH 9

RESULT 10  
US-10-168-185-8  
;; Sequence 8, Application US/10/168185  
;; Publication No. US20030175802A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Armbruster, Franz Paul  
;; APPLICANT: Missbichler, Albert  
;; APPLICANT: Schmidt-Gayk, Heinrich  
;; APPLICANT: Roth, Heinz-Jürgen  
;; TITLE OF INVENTION: Method for Determining Parathormone  
;; TITLE OF INVENTION: Activity in a Human Sample  
;; FILE REFERENCE: HLZ-004US  
;; CURRENT APPLICATION NUMBER: US/10/168,185  
;; CURRENT FILING DATE: 2002-06-17  
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911  
;; PRIOR FILING DATE: 2000-12-18  
;; PRIOR APPLICATION NUMBER: DE 19961350  
;; PRIOR FILING DATE: 1999-12-17  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 8  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-168-185-8

Query Match 69.5%; Score 41; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQLMHN 10  
DB 1 SEIQLMHN 8

RESULT 11  
US-10-192-673-7  
;; Sequence 7, Application US/10/192673  
;; Publication No. US20030166838A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gardella, Thomas J.  
;; APPLICANT: Kronenberg, Henry  
;; APPLICANT: Potts, John T.  
;; APPLICANT: Juppner, Harald  
;; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
;; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
;; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)



```
FILE REFERENCE: 0609.4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-192-673-7
```

```
Query Match
Best Local Similarity 67.8%; Score 40; DB 14; Length 9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVSEIQLMH 9
Db 1 SVSEIQLMH 9
```

```
RESULT 12
US-10-168-185-2
Sequence 2, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Miesbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jürgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-185-2
```

```
Query Match
Best Local Similarity 67.8%; Score 40; DB 14; Length 9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVSEIQLMH 9
Db 1 SVSEIQLMH 9
```

```
RESULT 13
US-10-192-673-8
Sequence 8, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
Parathyroid Hormone (PTH) and Parathyroid
```

```
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
FILE REFERENCE: 0609.4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-192-673-8
```

```
Query Match
Best Local Similarity 55.9%; Score 33; DB 14; Length 9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 AVSEIQLMH 9
Db 1 SVSEIQLMH 9
```

```
RESULT 14
US-10-168-185-3
Sequence 3, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Miesbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jürgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-185-3
```

```
Query Match
Best Local Similarity 54.2%; Score 32; DB 14; Length 8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AVSEIQLMH 8
Db 1 SVSEIQLMH 8
```

```
RESULT 15
US-10-192-673-10
Sequence 10, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
```

; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)  
; FILE REFERENCE: 0609.4570002  
; CURRENT APPLICATION NUMBER: US/10/192,673  
; CURRENT FILING DATE: 2002-07-11  
; PRIOR APPLICATION NUMBER: U.S. 09/421,379  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: U.S. 60/105,530  
; PRIOR FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO: 10  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
; US-10-192-673-10

Query Match 50.8%; Score 30; DB 14; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1e+06; 1; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9  
: ||| ||:  
Db 1 SVSEHQLTH 9

Search completed: May 18, 2004, 10:21:00  
Job time: 34.25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:58:45 ; Search time 12.75 Seconds  
(without alignment)

48.589 Million cell updates/sec

Title: US-09-730-174A-5  
Perfect score: 59  
Sequence: 1 AVSEIQLMHLNG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	53	89.8	12 4 US-09-442-989-31	Sequence 31, Appl
2	46	78.0	10 3 US-08-817-547A-1	Sequence 1, Appl
3	43	72.9	9 4 US-09-421-379-6	Sequence 6, Appl
4	40	67.8	9 3 US-08-817-547A-2	Sequence 2, Appl
5	40	67.8	9 4 US-09-421-379-7	Sequence 7, Appl
6	35	59.3	11 6 5460978-3	Patent No. 5460978
7	33	55.9	9 4 US-09-421-379-8	Sequence 8, Appl
8	32	54.2	9 3 US-08-817-547A-3	Sequence 3, Appl
9	30	50.8	9 4 US-09-421-379-10	Sequence 10, Appl
10	27	45.8	7 3 US-08-817-547A-4	Sequence 4, Appl
11	25	42.4	10 2 US-08-429-257A-14	Sequence 14, Appl
12	25	42.4	11 3 US-08-802-981-124	Sequence 124, App
13	24	40.7	5 2 US-08-177-109A-56	Sequence 56, Appl
14	24	40.7	5 2 US-08-687-706-56	Sequence 56, Appl
15	24	40.7	5 3 US-08-817-547A-17	Sequence 17, Appl
16	24	40.7	6 3 US-08-817-547A-16	Sequence 16, Appl
17	24	40.7	7 3 US-08-817-547A-15	Sequence 15, Appl
18	24	40.7	8 2 US-08-748-021-64	Sequence 64, Appl
19	24	40.7	8 3 US-08-817-547A-14	Sequence 14, Appl
20	24	40.7	8 3 US-08-974-297-64	Sequence 64, Appl
21	24	40.7	9 3 US-08-817-547A-13	Sequence 13, Appl
22	24	40.7	10 3 US-08-817-547A-7	Sequence 7, Appl
23	24	40.7	11 2 US-08-726-464B-13	Sequence 13, Appl
24	24	40.7	11 4 US-09-428-082B-41	Sequence 41, Appl
25	23	39.0	6 3 US-08-817-547A-5	Sequence 5, Appl
26	23	39.0	7 4 US-09-316-093-12	Sequence 12, Appl
27	23	39.0	7 4 US-09-557-465D-12	Sequence 12, Appl

28	23	39.0	10 3 US-08-396-385-6	Sequence 6, Appl
29	23	39.0	10 4 US-09-287-221-6	Sequence 6, Appl
30	23	39.0	12 2 US-08-140-137A-42	Sequence 42, Appl
31	23	39.0	12 4 US-08-474-349A-271	Sequence 271, App
32	22	37.3	8 3 US-08-160-604-74	Sequence 74, Appl
33	22	37.3	8 3 US-08-160-604-75	Sequence 75, Appl
34	22	37.3	8 4 US-09-296-089-10	Sequence 10, Appl
35	22	37.3	8 4 US-09-551-976-10	Sequence 10, Appl
36	22	37.3	9 4 US-08-492-543-177	Sequence 177, App
37	22	37.3	11 3 US-08-652-877-71	Sequence 71, Appl
38	22	37.3	11 3 US-08-160-604-73	Sequence 73, Appl
39	22	37.3	11 3 US-08-476-515A-71	Sequence 71, Appl
40	22	37.3	11 4 US-09-296-089-27	Sequence 27, Appl
41	22	37.3	11 4 US-08-475-955-56	Sequence 56, Appl
42	22	37.3	11 4 US-09-551-976-27	Sequence 27, Appl
43	22	37.3	12 4 US-09-690-454-89	Sequence 89, Appl
44	22	37.3	12 4 US-09-591-694-41	Sequence 41, Appl
45	21	35.6	6 2 US-08-621-803-184	Sequence 184, App

## ALIGNMENTS

RESULT 1  
US-09-442-989-31  
Sequence 31, Application US/09442989  
Patent No. 6563993  
GENERAL INFORMATION:  
APPLICANT: Sledeski, Adam W.  
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC  
FILE REFERENCE: A3113B-US  
CURRENT APPLICATION NUMBER: US/09/442,989  
CURRENT FILING DATE: 1999-11-18  
EARLIER APPLICATION NUMBER: 60/081,897  
EARLIER FILING DATE: 1998-04-15  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 31  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)  
OTHER INFORMATION: FMOC-Ala  
NAME/KEY: PEPTIDE  
LOCATION: (9)  
OTHER INFORMATION: His(Ttc)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (6)  
OTHER INFORMATION: Glu(Ttc)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (10)  
OTHER INFORMATION: Asn(Ttc)  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (8)  
OTHER INFORMATION: Nle  
US-09-442-989-31

Query Match 89.8%; Score 53; DB 4; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.0012;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQMLNMG 12  
DB 1 AVSEIQMLNMG 12

RESULT 2  
US-08-817-547A-1  
Sequence 1, Application US/08817547A

PATENT No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Ademann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Magerlein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHEICAL: no  
ANTI-SENSE: no  
US-08-817-547A-1

Query Match 78.0%; Score 46; DB 3; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.019;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQMLNMG 10  
DB 1 AVSEIQMLNMG 10

RESULT 3  
US-09-421-379-6  
Sequence 6, Application US/09421379  
PATENT No. 649562  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Krenenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald

TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)  
FILE REFERENCE: 0609,4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 6  
LENGTH: 9  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-421-379-6

Query Match 72.9%; Score 43; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQMLNMG 9  
DB 1 AVSEIQMLNMG 9

RESULT 4  
US-08-817-547A-2  
Sequence 2, Application US/08817547A  
PATENT No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Ademann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Magerlein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHEICAL: no  
ANTI-SENSE: no  
US-08-817-547A-2

Query Match 67.8%; Score 40; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 3e+05; 0;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9  
Db 1 AVSEIQLMH 9

RESULT 5  
US-09-421-379-7  
Sequence 7, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)  
FILE REFERENCE: 0609.4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 7  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-421-379-7

Query Match 67.8%; Score 40; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 3e+05; 0;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9  
Db 1 AVSEIQLMH 9

RESULT 6  
5460978-3  
Patent No. 5460978  
APPLICANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,  
BRUCE E.; WETTENHAL, RICHARD E.H.  
TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL  
HYPERCALCEMIA OF MALIGNANCY-PTHrP  
NUMBER OF SEQUENCES: 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/715,280  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 199,235  
FILING DATE: 09-MAY-1988  
APPLICATION NUMBER:  
FILING DATE:  
SEQ ID NO: 3;  
LENGTH: 11  
5460978-3

Query Match 59.3%; Score 35; DB 6; Length 11;  
Best Local Similarity 80.0%; Pred. No. 2.2; 0;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 10  
Db 1 AVSEIQLMH 10

Db 1 AVSEIQLMH 10

RESULT 7  
US-09-421-379-8  
Sequence 8, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)  
FILE REFERENCE: 0609.4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 8  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-421-379-8

Query Match 55.3%; Score 33; DB 4; Length 9;  
Best Local Similarity 77.8%; Pred. No. 3e+05; 0;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9  
Db 1 AVSEIQLMH 9

RESULT 8  
US-08-817-547A-3  
Sequence 3, Application US/08817547A  
Patent No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Adermann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Magerlein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHEICAL: no  
ANTI-SENSE: no  
US-08-817-547A-3

Query Match 54.2%; Score 32; DB 3; Length 8;  
Best Local Similarity 87.5%; Pred. No. 3e+05;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLM 8  
:|||||  
Db 1 SVSEIQLM 8

RESULT 9  
US-09-421-379-10  
Sequence 10, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kromberg, Henry  
APPLICANT: Potts, John T.  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
FILE REFERENCE: 0609 4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-421-379-10

Query Match 50.8%; Score 30; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQLM 9  
:|||||  
Db 1 SVSEIQLM 9

RESULT 10  
US-08-817-547A-4  
Sequence 4, Application US/08817547A  
Patent No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Adernann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Magglein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta

STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHEICAL: no  
ANTI-SENSE: no  
US-08-817-547A-4

Query Match 45.8%; Score 27; DB 3; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQ 7  
:|||||  
Db 1 SVSEIQ 7

RESULT 11  
US-08-428-257A-14  
Sequence 14, Application US/08428257A  
Patent No. 5885808  
GENERAL INFORMATION:  
APPLICANT: Spooner, Robert A.  
APPLICANT: Speneles, A.A.  
TITLE OF INVENTION: Compounds to target cells  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jules E. Goldberg  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10016-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EFO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,257A  
FILING DATE: 07/05/95  
CLASSIFICATION: 514  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-428-257A-14

Query Match 42.4%; Score 25; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 4 VSEIOL 7  
4 VSEIOL 9

RESULT 12  
US-08-802-981-124  
Sequence 124, Application US/08802981  
Patent No. 6037137  
GENERAL INFORMATION:  
APPLICANT: Komoriya, Akira  
TITLE OF INVENTION: Compositions for the Detection of Enzyme  
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof  
NUMBER OF SEQUENCES: 231  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 018685-000300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /Product= "A1b"  
US-08-802-981-124

Query Match 42.4%; Score 25; DB 3; Length 11;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 6 OLHN 10  
5 OLHN 9

RESULT 13  
US-08-177-109A-56  
Sequence 56, Application US/08177109A  
Patent No. 569645  
GENERAL INFORMATION:  
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby  
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES  
NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/177,109A  
FILING DATE: 03-JAN-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.

Query Match 40.7%; Score 24; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
DB 8 MENLG 12  
1 LHMWG 5

RESULT 14  
US-08-687-706-56  
Sequence 56, Application US/08687706  
Patent No. 592892  
GENERAL INFORMATION:  
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby  
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,706  
FILING DATE: 26-JUL-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: US 08/177,109  
FILING DATE: 03-JAN-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.

Tue May 18 12:03:07 2004

us-09-730-174a-5.closed.rat

Page 6

REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: WU 107 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
-HYPOTHETICAL: NO  
US-08-687-706-56

Query Match 40.7%; Score 24; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 8 HNLG 12  
DB 1 LHWG 5

RESULT 15  
US-08-817-547A-17  
Sequence 17, Application US/08817547A  
Patent No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Adermann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Magerlein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-817-547A-17

Query Match 40.7%; Score 24; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 9 HNLG 12  
DB 1 HNLG 4

Search completed: May 18, 2004, 10:06:44  
Job time : 12.75 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:56:10 ; Search time 10.25 Seconds  
(without alignments)  
112.614 Million cell updates/sec

Title: US-09-730-174a-6  
Perfect score: 61  
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR 78: \*  
2: PIR1: \*  
3: PIR2: \*  
4: PIR3: \*  
5: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	32.8	10	2	S28055 cytochrome b559 co
2	20	32.8	12	2	PH1187 T-cell receptor al
3	18	29.5	7	2	A58718 carnosin u49 - Ca
4	18	29.5	9	2	S78420 ribosomal protein
5	18	29.5	10	2	A60589 sperm-activating p
6	18	29.5	12	2	PH1190 T-cell receptor al
7	17	27.9	8	2	A05169 neuropeptide M-I
8	17	27.9	10	2	A37268 Ig heavy chain C r
9	17	27.9	12	1	A43975 locustamytroptin -
10	17	27.9	12	1	S21205 Ig heavy chain V r
11	17	27.9	12	2	PH1189 T-cell receptor al
12	16	26.2	7	2	A46868 alpha-myosin heavy
13	16	26.2	10	2	UC1416 hypertrehalosemic
14	16	26.2	10	2	S09138 hypertrehalosemic
15	16	26.2	11	2	A32428 amine oxidase (cop
16	15	24.6	7	2	S29735 polyphosphate-glu
17	15	24.6	9	2	PT0231 Ig heavy chain CDR
18	15	24.6	9	2	A56029 N-methylpurine DNA
19	15	24.6	10	2	S33844 alpha-2-macroglobu
20	15	24.6	10	2	S38304 lectin GNL1 alpha
21	15	24.6	11	2	E49033 T-cell receptor ga
22	15	24.6	11	2	A38841 rhodopsin homolog
23	15	24.6	12	2	A55837 5-aminimidazole r
24	15	24.6	12	2	PH1174 T-cell receptor al
25	15	24.6	12	2	SM1737 T-cell receptor be
26	14	23.0	4	2	A57779 neuropeptide Antho
27	14	23.0	7	2	S78024 ribosomal protein
28	14	23.0	8	2	S08995 hypertrehalosemic
29	14	23.0	8	2	A49823 adipokinetic hormo

30	14	23.0	8	2	A44560 neuropeptide led-C
31	14	23.0	9	2	PM0002 chlorophyll a/b-bi
32	14	23.0	9	2	PT0238 Ig heavy chain CRD
33	14	23.0	10	1	SPPGNK neuromedin K - p19
34	14	23.0	10	2	S27873 hypothetical prote
35	14	23.0	10	2	C61033 ranatachykrin C -
36	14	23.0	10	2	B46453 e antigen p20e pre
37	14	23.0	10	2	C44787 calliFERamide 12
38	14	23.0	11	2	B41835 translation elonga
39	14	23.0	11	2	S19301 endo-1,4-beta-xyla
40	14	23.0	11	2	PA0028 protein QA300042 -
41	14	23.0	11	2	S60354 retinal oxidase -
42	14	23.0	11	2	S51436 beta-D-galactosida
43	14	23.0	12	2	S25485 transcription fact
44	14	23.0	12	2	S71034 potB protein - Sal
45	14	23.0	12	2	PH1175 T-cell receptor al

## ALIGNMENTS

## RESULT 1

S28055 cytochrome b559 component psbf - pepper chloroplast (fragment)  
C:Species: chloroplast Capsicum annuum (pepper)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-Jun-1999  
C:Accession: S28055  
R:Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.  
Plant Mol. Biol. 20, 1185-1188, 1992  
A:Title: The psbL gene from bell pepper (Capsicum annuum): plastid RNA editing also occu  
A:Reference number: S28055; MUID:93092270; PMID:1463853  
A:Accession: S28055  
A:Molecule type: DNA  
A:Residues: 1-10 <KUN>  
A:Cross-References: EMBL:X65570; NID:G14344; PIDD:CAA46539.1; PIDD:G415734  
C:Genetics:  
A:Gene: psbf  
A:Genome: chloroplast  
C:Superfamily: cytochrome b559 component F  
C:Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match 32.8%; Score 20; DB 2; Length 10;  
Best Local Similarity 37.5%; Pred. No. 7.4e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFM 8  
DB 1 SISAMQFI 8

## RESULT 2

PH1187 T-cell receptor alpha chain V region (Cw3/1F11) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH1187  
R:Casanova, J.L.; Cerottini, J.C.; Mathis, M.; Necker, A.; Gournier, H.; Barra, C.; Wic  
J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A:Reference number: S26512; MUID:92364546; PMID:1380061  
A:Accession: PH1187  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>

Query Match 32.8%; Score 20; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 9.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIQFM 7  
DB 2 AVSEIQFM 8

## RESULT 3

A58718

carnocin Uf49 - Carnobacterium sp. (fragment)

C/Species: Carnobacterium sp. (fragment)

C/Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998

C/Accession: A58718

R/Species: Rattus norvegicus (Norway rat)

C/Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000

C/Accession: S78420

R/Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A/Reference number: S78411

A/Accession: S78420

A/Molecule type: protein

A/Residues: 1-9 &lt;COL&gt;

A/Note: the protein is designated as mitochondrial ribosomal protein L41

C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match

Best Local Similarity 29.5%; Score 18; DB 2; Length 7;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6

Db 2 SEIQ 5

## RESULT 4

S78420

ribosomal protein R41, mitochondrial [validated] - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000

C/Accession: S78420

R/Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A/Reference number: S78411

A/Accession: S78420

A/Molecule type: protein

A/Residues: 1-9 &lt;COL&gt;

A/Note: the protein is designated as mitochondrial ribosomal protein L41

C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match

Best Local Similarity 29.5%; Score 18; DB 2; Length 9;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12

Db 5 HRLG 8

## RESULT 5

A60589

sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchin

C/Species: Heterocentrotus mamillatus

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000

C/Accession: A60589

R/Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi, K.

Comp. Biochem. Physiol. B 94, 739-751, 1989

A/Title: A halogenated amino acid-containing sperm activating peptide and its related peptides

A/Reference number: A60527

A/Accession: A60589

A/Molecule type: protein

A/Residues: 1-10 &lt;YOS&gt;

C/Suprafamily: unassigned animal peptides

Query Match

Best Local Similarity 29.5%; Score 18; DB 2; Length 10;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNLG 12

Db 2 YNLG 5

## RESULT 6

PH1190

T-cell receptor alpha chain V region (Cv3/10.1) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C/Accession: PH1190

R/Caenova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Widmer, J.

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A/Reference number: S26512; PMID:92364546; PMID:1380061

A/Accession: PH1190

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-12 &lt;CAS&gt;

Query Match

Best Local Similarity 29.5%; Score 18; DB 2; Length 12;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIQ 7

Db 2 AVSEHG 8

## RESULT 7

A05169

neuropeptide M-I - American cockroach

C/Species: Periplaneta americana (American cockroach)

C/Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Dec-1993

C/Accession: A05169

R/Wilten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.

Biochem. Biophys. Res. Commun. 124, 350-358, 1984

A/Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass

A/Reference number: A90118; PMID:85046530; PMID:6548628

A/Accession: A05169

A/Molecule type: protein

A/Residues: 1-8 &lt;MT&gt;

C/Keywords: neuropeptide

Query Match

Best Local Similarity 27.9%; Score 17; DB 2; Length 8;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 EIOFMEN 10

Db 1 EVNFSN 7

## RESULT 8

A37268

Ig heavy chain C region (129) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998

C/Accession: A37268

R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A/Title: Heavy and light chain variable region sequences and antibody properties of anti

A/Reference number: A38740; PMID:91177923; PMID:1706720

A/Accession: A37268

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-10 &lt;RUF&gt;

Query Match

Best Local Similarity 27.9%; Score 17; DB 2; Length 10;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIOFMEN 12

Db 1 ESQSPNVG 9

## RESULT 9

locustamytropin - migratory locust  
A43975  
N/Alternate names: Lom-WT  
C/Species: Locusta migratoria (migratory locust)  
C/Date: 11-Feb-1993 #sequence\_revision 02-Jun-1994 #text\_change 08-Dec-1995  
C/Accession: A43975  
R/Schoofs, L.; Holman, G.M.; Hayes, T.K.; Tjips, A.; Nachman, R.J.; Vandesande, F.; De Le  
Peptides 11, 427-433, 1990  
A/Title: Isolation, identification and synthesis of locustamytropin (Lom-WT), a novel h  
A/Reference number: A43975; PMID:90341077; PMID:1974346  
A/Accession: A43975  
A/Molecule type: protein  
A/Residues: 1-12 <SCH>  
A/Note: the amino end of this peptide is not blocked  
C/Comment: Synthetic locustamytropin mimics natural locustamytropin only in the amidated  
C/Superfamily: Pyrokinin  
C/Keywords: amidated carboxyl end; neuropeptide  
F/12/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 27.9%; Score 17; DB 1; Length 12;  
Best Local Similarity 45.5%; Pred. No. 3.5e+03;  
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 AVSEIQFMNLT 11  
Db 2 AVPAQFSPRL 12

## RESULT 10

S21205  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C/Accession: S21205  
R/Makiya, R.; Scigbrand, T.  
Eur. J. Biochem. 205, 341-345, 1992  
A/Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin-  
A/Reference number: S21205; PMID:92209522; PMID:1555592  
A/Accession: S21205  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12 <MA>  
C/Keywords: heterotrimer; immunoglobulin

Query Match 27.9%; Score 17; DB 2; Length 12;  
Best Local Similarity 33.3%; Pred. No. 3.5e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 EIQFMNLTG 12  
Db 1 EVQLVESG 9

## RESULT 11

PH1189  
T-cell receptor alpha chain V region (Cw3/2C3) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1189  
R/Casanova, J.L.; Gerotini, J.C.; Matches, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
J. Exp. Med. 176, 439-447, 1992  
A/Title: H-2-restricted cytoolytic T lymphocytes specific for HLA display T cell receptor  
A/Reference number: S26512; PMID:92364546; PMID:1380061  
A/Accession: PH1189  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-12 <CAS>

Query Match 27.9%; Score 17; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVSE 4  
Db 2 AVSE 5

## RESULT 12

alpha-myosin heavy chain - rabbit (fragment)  
I46868  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 05-Nov-1999  
C/Accession: I46868  
R/Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.  
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984  
A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula  
A/Reference number: I46868; PMID:84221901; PMID:6528451  
A/Accession: I46868  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-7 <FR1>  
A/Cross-references: GB:K01698; NID:G165538; PIDN:AAA11415.1; PID:G165539

Query Match 26.2%; Score 16; DB 2; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 QFMN 10  
Db 1 QFMND 5

## RESULT 13

JC1416  
hypertrehalosemic hormone I - stick insect (Carausius morosus)  
N/Alternate names: neuropeptide Cam-HrTH-I  
N/Contains: hypertrehalosemic factor II  
C/Species: Carausius morosus  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: JC1416; S07157  
R/Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.  
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992  
A/Title: A tryptophan-substituted member of the AKH/RPH family isolated from a stick in  
A/Reference number: JC1416; PMID:93129186; PMID:1482345  
A/Accession: JC1416  
A/Molecule type: protein  
A/Residues: 1-10 <GAE1>  
R/Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 368, 67-75, 1997  
A/Title: Primary structure of the hypertrehalosemic factor II from the corpus cardiacu  
A/Reference number: S07157; PMID:87157103; PMID:3828078  
A/Accession: S07157  
A/Molecule type: protein  
A/Residues: 1-10 <GAE2>  
C/Comment: Hypertrehalosemic factor II lacks the tryptophan modification.  
C/Comment: This peptide raises hemolymph levels of trehalose in the cockroach periplanet  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic aci  
F/1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
F/8/Binding site: carboxylate (Trp) (covalent) #status experimental  
F/10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 26.2%; Score 16; DB 2; Length 10;  
Best Local Similarity 33.3%; Pred. No. 4.5e+03;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 4 EIQFMNLTG 12  
Db 1 QLTFTPMWG 9

## RESULT 14

S09138

hypertrehalosemic hormone II - stick insect (Extratosoma tiaratum)  
 N/Alternate names: Cam-HrTH-II  
 C/Species: Extratosoma tiaratum  
 C/Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997  
 C/Accession: S09138  
 R/Gaele, G.; Rinehart, K.L.  
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
 A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extratosoma tiaratum assigned by tandem fast atom bombardment  
 A/Reference number: S08995; MUID:90253659; PMID:2340112  
 A/Accession: S09138  
 A/Molecule type: protein  
 A/Residues: 1-10 <GAE>  
 A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have C/Superfamily: adipokinetic hormone  
 C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F/10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 26.2%; Score 16; DB 2; Length 10;  
 Best Local Similarity 33.3%; Pred. No. 4.5e+03;  
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 4 EIQPMHNG 12  
 ::|  
 Db 1 QLTFTPMWG 9

## RESULT 15

A32428  
 A/Name: amine oxidase (copper-containing) (EC 1.4.3.6) - pig (fragment)  
 C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 12-Oct-1989 #sequence\_revision 31-Dec-1993 #text\_change 06-Sep-1996  
 C/Accession: A32428  
 R/van der Meer, R.A.; van Massenaar, P.D.; van Brouwershaven, J.H.; Duine, J.A.  
 Biochem. Biophys. Res. Commun. 159, 726-733, 1989  
 A/Title: Primary structure of a pyrroloquinoline quinone (PQQ) containing peptide isolated from the pig  
 A/Reference number: A32428; MUID:89193662; PMID:2539124  
 A/Accession: A32428  
 A/Molecule type: protein  
 A/Residues: 1-7, 'K', 9-11 <VAN>  
 A/Note: the modified residue thought by the authors to be pyrroloquinoline quinone covalently bound to the protein  
 C/Keywords: oxidoreductase; quinoprotein; topaquinone  
 F/8/Modified site: topaquinone (Tyr) #status predicted

Query Match 26.2%; Score 16; DB 2; Length 11;  
 Best Local Similarity 37.5%; Pred. No. 5e+03;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 SEIOFMHN 10  
 |::|  
 Db 2 SDAVFTVN 9

Search completed: May 18, 2004, 10:05:41  
 Job time : 10.25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

```
Run on:      May 18, 2004, 09:43:45 ; Search time 6.75 Seconds
              (without alignments)
              92.569 Million cell updates/sec
```

Title: US-09-730-174A-6  
Perfect score: 61  
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

```

Searched:      141681 segs, 52070155 residues
Total number of hits satisfying chosen parameters:  501

```

```
Minimum DB seq length: 0
Maximum DB seq length: 12
```

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	32.8	10	1	PSBF_CAVAN	Q03367 capsicum an
2	18	29.5	7	1	LANC_CARUI	P36560 carnobacter
3	18	29.5	10	1	HTF1_ROMMI	P18110 romalea mid
4	17	27.9	12	1	LMT1_LOOMI	P23995 locusta mig
5	16	26.2	8	1	ALF6_CYPPO	P82157 cydia pomon
6	16	26.2	10	1	HTF2_CAVNO	P11355 carastusius m
7	15	24.6	5	1	EIO3_LITRU	P82099 litorea rub
8	15	24.6	8	1	FUSS_FUSSO	P81040 fusarium so
9	15	24.6	11	1	EFEG_CLOPA	P81330 fusarium sc
10	15	24.6	11	1	NUHM_CAMEA	P49820 canis famli
11	14	23.0	4	1	FLRN_ANELI	P58707 anthropleura
12	14	23.0	7	1	ALL7_CYPPO	P82158 cydia pomon
13	14	23.0	7	1	LYS1_LITRU	P82065 litorea rub
14	14	23.0	8	1	AL18_CAVMA	P81821 carcinus ma
15	14	23.0	8	1	ALL1_CYPPO	P82152 cydia pomon
16	14	23.0	8	1	HTF1_PEPAM	P04548 periplaneta
17	14	23.0	9	1	FAR8_MACRS	P83281 macrobrachi
18	14	23.0	9	1	UF02_MOISE	P38640 mus musculi
19	14	23.0	10	1	ALL5_CAVMA	P81822 carcinus ma
20	14	23.0	10	1	FAR2_PENNO	P83317 penaeus mon
21	14	23.0	10	1	FARC_CALPHO	P41867 calliphora
22	14	23.0	10	1	TKNC_PANCA	P22650 rana catesb
23	14	23.0	10	1	TKNC_PIG	P01292 sus scrofa
24	14	23.0	11	1	ASL1_BACSE	P83146 bacteroides
25	14	23.0	11	1	PORD_MATM	P80993 metanobact
26	14	23.0	12	1	RS19_TOBBP	Q56251 tomato big
27	13	21.3	6	1	TRP1_PEPBU	P36414 pseudomona
28	13	21.3	8	1	HTF_TENNO	P25419 tenebrio mo
29	13	21.3	8	1	LCK4_LEIMA	P21143 leucophaea
30	13	21.3	8	1	LCK6_LEIMA	P19988 leucophaea
31	13	21.3	9	1	CONO_CONGE	P05466 conus geogr
32	13	21.3	9	1	MOSH_CUXJA	P19852 clypeaster
33	13	21.3	9	1	OXYT_EISFO	P42998 eisenia foe

34	13	21.3	9	1	ASPL1	PERAM	P82631	periplaneta
35	13	21.3	11	1	CS11.7	BACSE	P83147	bacterioides
36	13	21.3	11	1	CONZ2	PERAM	P11466	periplaneta
37	13	21.3	11	1	CS15	BACGU	P11055	dacilius
38	13	21.3	11	1	PVK1	PERAM	P41837	periplaneta
39	13	21.3	11	1	Q20A	COMTE	P80464	comatomas
40	13	21.3	12	1	UKA2	HUMAN	P11144	homo sapiens
41	12	19.7	5	1	RE21	LITRU	P82071	litoria
42	12	19.7	5	1	RE31	LITRU	P82072	litoria
43	12	19.7	8	1	ANG2	BOTUA	Q10582	bothrops
44	12	19.7	8	1	HTF2	PERAM	P41589	periplaneta
45	12	19.7	9	1	F1B5	ERYPA	P19346	erythrocebus

## ALIGNMENTS

```

RESULT 1
ID      PSBF_CAPAN      STANDARD;      PRT;      10 AA.
AC      003357;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Cytochrome b559 beta subunit (PSII reaction center subunit VI
      (Fragment)).
GN      PSBF
OS      Capsicum annuum (Bell pepper).
OC      Chloroplast.
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC      lamiales; Solanales; Solanaceae; Capsicum.
OX      NCBI_TaxID=4072;
      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Lamuyo, TISSUE=fruit, and leaf;
RA      MEDLINE=9309270; PubMed=146353;
RX      Kuntz M., Camara B., Weil J.-H., Schantz R.;
RT      "The psbI gene from bell pepper (Capsicum annuum): plastid RNA
      editing also occurs in non-photosynthetic chromoplasts."
RL      Plant Mol. Biol. 20:1185-1188(1992).
CC      -1- FUNCTION: This b-type cytochrome is tightly associated with the
      reaction center of photosystem II and possibly is part of the
      water-oxidation complex.
CC      -1- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC      -1- SIMILARITY: Belongs to the psbE / psbF family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X65570; CAA46539.1; -.
DR      F1R; S28055; S28055.
DR      HAMAP; MF_00643; -; 1.
DR      InterPro; IPR006216; Cyt_b559.
DR      PROSITE; PS00537; CYTOCHROME_B559; PARTIAL.
KW      Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT      NON TER      1      1
FT      TRANSMEM      <1      5
FT      DOMAIN      6      10      LUMENAL (POTENTIAL).
SQ      SEQUENCE      10 AA; 1180 MM; 8170F59D6D69DC5 CRC64;
Query Match      32.8%; Score 20; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 4.8e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0
Oy      1 AVS3IQFM 8
      ::|::|:
      1 SISAMQFI 8

```

```

RESULT 2
ID LANC_CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin U149 (Fragment).
OS Carnobacterium sp. (strain U149).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -1- FUNCTION: Lantionine-containing peptide antibiotic (lantibiotic).
CC Active on Gram-positive bacteria.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON TER
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 29.5%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEQ 6
Db 2 SEQ 5

RESULT 3
HTFL_ROMMI
ID HTFL_ROMMI STANDARD; PRT; 10 AA.
AC P1810;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RO I (Hypertrehalosemic factor).
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caellifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
NCBI_TaxID=7007;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the ACH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -1- FUNCTION: Hypertrehalosemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC Intrapro: IPR002047; AKH.
DR PROSITE; PS00256; AKH, 1.
KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
SQ MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;

Query Match 29.5%; Score 18; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 4 EIQFVHNLG 12
Db 1 QVNFEPNMG 9

RESULT 4
ID LMT1_LOCMI STANDARD; PRT; 12 AA.
AC P22395;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Locustamyotropin 1 (LOM-MT-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caellifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
RX MEDLINE=90341077; PubMed=1974346;
RA Schoofs L., Holman G.W., Hayes T.K., Tips A., Nachman R.J.,
RA Vandesaende F., de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin
RT (LOM-MT), a novel biologically active insect peptide.";
RL Peptides 11:427-433(1990).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SIMILARITY: Belongs to the pyrokinin family.
CC PIR; A43975; A43975.
DR InterPro; IPR001484; PYROKININ.
DR PROSITE; PS00539; PYROKININ, 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1213 MW; D76EC92722D6DD CRC64;

Query Match 27.9%; Score 17; DB 1; Length 12;
Best Local Similarity 45.5%; Pred. No. 2.3e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AVSEIQFHNH 11
Db 2 AVPAQFSPRL 12

RESULT 5
ID ALLE_CYDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydistactin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RX TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duvé H., Johnsen A.H., Maestre J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

```

Query Match 26.2%; Score 16; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MNHNG 12  
 DB 3 LYNFG 7

RESULT 6  
 HTF2\_CARMO STANDARD; PRT; 10 AA.  
 ID HTF2\_CARMO  
 AC P1385;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypertrehalosaemic factor II (HTF-II) (HRTN-II) (Hypertrehalosaemic neuropeptide II).  
 OS Carausius morosus (Indian stick insect), and  
 OS Ectatosoma tiaratum (Stick insect).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Phasmatoidea; Euphasmida; Phasmatodea;  
 OC Heteronemiidae; Carausius.  
 NCBI\_TaxID=7022, 7024;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;  
 RX MEDLINE=87157103; PubMed=3828078;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structure of the hypertrehalosaemic factor II from the corpus cardiaca of the Indian stick insect, Carausius morosus, determined by fast atom bombardment mass spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90253659; PubMed=2340112;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora cardiaca of the cockroaches Leucophaea maderae, Gromphadorhina portentosa, Blattella germanica and Blatta orientalis and of the stick insect Ectatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
 RN [3]  
 RP CARBOHYDRATE-LINKAGE SITE.  
 RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;  
 RX MEDLINE=3129188; PubMed=1482345;  
 RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;  
 RT "A tryptophan-substituted member of the AKH/RPH family isolated from a stick insect corpus cardiaca.";  
 RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).  
 CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that elevate the level of trehalose in the hemolymph (trehalose is the major carbohydrate in the hemolymph of insects).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MASS SPECTROMETRY: MW=1308.61; METHOD=FA-MS.  
 CC -1- SIMILARITY: Belongs to the AKH / RHTN / RPH family.  
 DR PIR; UCI416; UCI416.  
 DR PIR; S09138; S09138.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KM Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT CARBOXYD 8 8 C-LINKED (MAN) (PROBABLE).  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;

Query Match 26.2%; Score 16; DB 1; Length 10;  
 Best Local Similarity 33.3%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 4 EIOFMNNG 12

Db 1 QLTFTPNWG 9

RESULT 7  
 ID EIO3\_LITRU STANDARD; PRT; 5 AA.  
 AC P82059;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Electrin 3.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyliidae;  
 OC Pelodyadinae; Litoria.  
 NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog Litoria electrica. Comparison with the skin peptides from Litoria rubella.";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 KM Amphibian defense peptide; Amidation.  
 FT MOD\_RES 5 5 AMIDATION.  
 SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FMH 9  
 DB 1 FVH 3

RESULT 8  
 ID FUSO\_FUSO STANDARD; PRT; 8 AA.  
 AC P81010;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Allergen Fus s 13596\* (Fragment).  
 OS Fusarium solani (subsp. pisi) (Necrotia haematococca).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 CC Hypocnemycetidae; Hypocreales; Nectriaceae; Nectria.  
 NCBI\_TaxID=70791;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=IARI 3596; TISSUE=Mycelium;  
 RA Verma J., Gangal S.V.;  
 RT Submitted (JUL-1997) to Swiss-Prot.  
 CC -1- ALLERGEN: Causes an allergic reaction in human.  
 KM Allergen.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNL 11  
 DB 5 HNV 7

RESULT 9  
 EFG\_CLOPA

```

ID  EFG_CLOPA      STANDARD;      PRT;      11 AA.
AC  P81350;
DT  15-JUN-1998 (Rel. 36, Last sequence update)
DT  15-JUN-1998 (Rel. 36, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Elongation factor G (EF-G) (CP 5) (Fragment).
GN  FUSA.
OS  Clostridium pasteurianum.
OC  Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC  Clostridium.
OX  NCBI_TaxID=1501;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=WS;
RX  MEDLINE=98291870; PubMed=9629918;
RA  Flengstrand R., Skjeldal L.;
RT  "Two-dimensional gel electrophoresis separation and N-terminal
RL  sequence analysis of proteins from Clostridium pasteurianum WS.";
CC  Electrophoresis 19:802-806(1998).
CC  -1- FUNCTION: This protein promotes the GTP-dependent translocation of
CC  the nascent protein chain from the A-site to the P-site of the
CC  ribosome.
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
DR  InterPro: IPR000795; EF_GTPbind.
DR  PROSITE: PS00301; EFACITOR_GTP_PARTIAL.
KM  Elongation factor; Protein biosynthesis; GTP-binding.
FT  NON_TER
FT  11
SQ  SEQUENCE 11 AA; 1337 MW; 412E71F1D9C3B17 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 11;
Best Local Similarity 25.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY  5 IOFMHNG 12
    : : :
Db  4 LEKQNTG 11

RESULT 10
NUHM CANFA      STANDARD;      PRT;      11 AA.
AC  P49820;
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUN-1998 (Rel. 36, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE  (EC 1.6.99.3) (Fragment).
GN  NDUFV2.
OS  Canis familiaris (Dog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX  NCBI_TaxID=9615;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Heart;
RX  MEDLINE=98163340; PubMed=9504812;
RA  Dunn W.J., Corbett J.M., Wheeler C.H.;
RT  "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT  dog heart proteins.";
RL  Electrophoresis 18:2795-2802(1997).
CC  -1- FUNCTION: TRANSFER OF ELECTRON ACCEPTOR FROM NADH TO THE RESPIRATORY
CC  CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC  TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
CC  FRAGMENT OF THE ENZYME.
CC  -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC  -1- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC  -1- COFACTOR: Binds 1 2Fe-2S cluster (potential).
CC  -1- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC  -1- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
CC  mitochondrial inner membrane.
CC  -1- SIMILARITY: Belongs to the complex I 24 kDa subunit family.

```

```

DR  HSC-2DPAGE; P49820; DOG.
DR  InterPro: IPR002023; Cmplx1_24kDa.
DR  PROSITE: PS01099; COMPLEX1_24K; PARTIAL.
KM  Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
KM  Iron-sulfur; Iron; 2Fe-2S.
FT  NON_TER
FT  11
SQ  SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 5.1e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY  7 FMH 9
    : :
Db  7 FVH 9

RESULT 11
FLRN ANTEL
ID  FLRN ANTEL      STANDARD;      PRT;      4 AA.
AC  P58707;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Antho-RNamide.
OS  Anthopleura elegantissima (Sea anemone).
OC  Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC  Nymathea; Actinidae; Anthopleura.
OX  NCBI_TaxID=6110;
RN  [1]
RP  SEQUENCE, AND MASS SPECTROMETRY.
RX  MEDLINE=90319122; PubMed=1973541;
RA  Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA  Reinscheid R.K., Norbaker H.-P., Staley A.L.;
RT  "Isolation of L-3-phenylacetyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
RT  anemone neuropeptide containing an unusual amino-terminal blocking
RT  group.";
RL  Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- TISSUE SPECIFICITY: Neuron specific.
CC  -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAE.
DR  PIR; A35779; A35779.
KM  Neuropeptide; Amidation.
FT  MOD_RES
FT  1
FT  MOD_RES
FT  4
SQ  SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY  7 FMHN 10
    : :
Db  1 FLRN 4

RESULT 12
ALL7 CYDPO
ID  ALL7 CYDPO      STANDARD;      PRT;      7 AA.
AC  P82158;
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  30-MAY-2000 (Rel. 39, Last annotation update)
DE  Cydia pomonella (Coddling moth).
OS  Cydia pomonella (Coddling moth).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Lepidoptera; Glossata; Ditylidae;
OC  Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX  NCBI_TaxID=82600;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Larva;
RX  MEDLINE=98054539; PubMed=9392829;

```



RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Duvé H., East P.D., Thorpe A.,  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 CC Neuropeptide; Amidation.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 7  
 SQ SEQUENCE 7 AA; 873 MW; 672879CAB569350 CRC64;  
 Query Match 23.0%; Score 14; DB 1; Length 7;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 HNMG 12  
 DB 2 MYDFG 6  
 RESULT 13  
 TY51 LITRU STANDARD; PRT; 7 AA.  
 ID TY51 LITRU  
 AC P82065;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Trypophyllin 5.1.  
 OS Litoria rubella (Desert tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 CC Pelodytidae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Steinhorn S.T., Wabnitz P.A., Maugh R.V., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT of evolutionary trends of amphibians."  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=965; METHOD=FAE.  
 KW Amphibia defense peptide; Amidation; Neuropeptide;  
 KW Pyroglutamate carboxylic acid. PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD RES 1  
 FT MOD RES 7  
 SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;  
 Query Match 23.0%; Score 14; DB 1; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 EIOFMH 9  
 DB 1 QIPWFH 6  
 RESULT 14  
 AL18 CARMA STANDARD; PRT; 8 AA.  
 ID AL18 CARMA  
 AC P81821;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinostatin 18.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubranchyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaro P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas."  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 CC Neuropeptide; Amidation; Multigene family.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 919 MW; C62879D5B569A5 CRC64;  
 Query Match 23.0%; Score 14; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 HNMG 12  
 DB 3 MYDFG 7  
 RESULT 15  
 ALL1 CYDPO STANDARD; PRT; 8 AA.  
 ID ALL1 CYDPO  
 AC P82152;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiaastatin 1.  
 OS Cydia pomonella (Coddling moth).  
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Duvé H., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 CC Neuropeptide; Amidation.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 934 MW; C62879C45B51F775 CRC64;  
 Query Match 23.0%; Score 14; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 9 HNMG 12  
 DB 4 YNFG 7  
 Search completed: May 18, 2004, 10:02:34  
 Job time : 6.75 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 09:55:20 ; Search time 30.25 Seconds  
(without alignments)  
125.164 Million cell updates/sec

Title: US-09-730-174A-6

Perfect score: 61

Sequence: 1 ANSEIQFWHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues 2565

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeop:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	39.3	11	13 Q9PS71	Q9PS71 agkistrodon
2	19	31.1	8	6 Q9TT78	Q9TT78 canis fam1
3	19	31.1	9	12 Q92766	Q92766 canine dist
4	19	31.1	9	12 Q71066	Q71066 canine dist
5	19	31.1	12	13 P82081	P82081 limodysnat
6	18	29.5	8	3 Q13591	Q13591 saccharomyc
7	18	29.5	12	8 Q8MS0	Q8MS0 anoda crist
8	18	29.5	12	15 Q85631	Q85631 avian carci
9	17	27.9	11	5 Q23876	Q23876 dicystocell
10	17	27.9	12	13 P82085	P82085 limodysnat
11	16	26.2	7	6 Q28742	Q28742 oryctolagus
12	16	26.2	8	3 Q05403	Q05403 saccharomyc
13	16	26.2	8	10 Q40659	Q40659 cryza sativ
14	16	26.2	8	13 P82082	P82082 limodysnat
15	16	26.2	8	13 P82083	P82083 limodysnat
16	16	26.2	9	2 Q44377	Q44377 aeromonas t

17	16	26.2	9	2 Q44468	Q44468 aeromonas v
18	16	26.2	9	2 Q8RXU3	Q8RXU3 borrelia bu
19	16	26.2	9	2 Q43928	Q43928 aeromonas p
20	16	26.2	9	2 Q44001	Q44001 aeromonas e
21	16	26.2	9	10 Q9FX10	Q9FX10 111ium long
22	16	26.2	10	10 P82132	P82132 spinacia ol
23	16	26.2	10	10 P82133	P82133 spinacia ol
24	16	26.2	11	8 Q9GD68	Q9GD68 elaeis guin
25	16	26.2	11	10 P82336	P82336 pisum sativ
26	15	24.6	8	4 Q15894	Q15894 homo sapien
27	15	24.6	8	8 Q34909	Q34909 locusta mig
28	15	24.6	8	13 Q90493	Q90493 eopsaltria
29	15	24.6	9	2 Q43960	Q43960 azotobacter
30	15	24.6	9	4 Q15891	Q15891 homo sapien
31	15	24.6	9	10 Q853C6	Q853C6 glycine max
32	15	24.6	9	10 Q9RECO	Q9RECO hordeum vul
33	15	24.6	10	4 Q15342	Q15342 homo sapien
34	15	24.6	10	5 P82222	P82222 bombyx mori
35	15	24.6	10	10 Q8GZC8	Q8GZC8 hordeum vul
36	15	24.6	11	4 Q9C057	Q9C057 homo sapien
37	15	24.6	11	6 Q9BD09	Q9BD09 pongo pygma
38	15	24.6	11	6 Q9BD09	Q9BD09 gorilla gor
39	15	24.6	11	6 Q9BD09	Q9BD09 pan troglod
40	15	24.6	11	6 Q9BD09	Q9BD09 pan paniscu
41	15	24.6	12	4 Q9UNV5	Q9UNV5 homo sapien
42	14	23.0	7	8 Q9J182	Q9J182 gnatholebia
43	14	23.0	8	2 Q49534	Q49534 mycoplasma
44	14	23.0	8	12 Q84156	Q84156 orf virus (
45	14	23.0	8	13 Q91098	Q91098 manorina me

#### ALIGNMENTS

RESULT 1					
Q9PS71		PRELIMINARY;	PRT;	11 AA.	
AC Q9PS71;					
DT 01-MAY-2000 (TREMBlrel. 13, Created)					
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)					
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)					
DE Fibrinolytic metalloproteinase (Fragment).					
OS Agkistrodon contortrix.					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;					
OC Viperidae; Crotalinae; Agkistrodon.					
OX NCBI_Taxid=8720;					
RM [1]					
RP SEQUENCE.					
RX MEDLINE=91378546; Pubmed=1898066;					
RA Guan A.L., Reizios A.D., Henderson G.N., Markland F.S.Jr.;					
RT "Purification and characterization of a fibrinolytic enzyme from venom					
RT of the southern copperhead snake (Agkistrodon contortrix					
RT contortrix)." ;					
RL Arch. Biochem. Biophys. 289:197-207(1991).					
FT NON TER	11	11			
FT SEQUENCE	11 AA;	1209 MW;	7CA02D1D41E8772B CRC64;		
Query Match	39.3%;	Score 24;	DB 13;	Length 11;	
Best Local Similarity	100.0%;	Pred. No. 6.3e-02;			
Matches	4;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	9	HNLG 12			
DB	7	HNLG 10			
RESULT 2					
Q9TT78		PRELIMINARY;	PRT;	8 AA.	
ID Q9TT78					
AC Q9TT78;					
DT 01-MAY-2000 (TREMBlrel. 13, Created)					
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)					

```

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Thymidylate synthase (Fragment).
GN TS
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015404; Pubmed=11130975;
RA Brouillette J.A., Andrew J.R., Venta P.J.;
RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
method."
RL Mamm. Genome 11:1079-1086(2000).
DR EMBL; AF202073; AAF20918.1; -.
FT NON TER 1 1
FT SEQUENCE 8 AA; 899 MW; 6731AE059CAA867 CRC64;
SQ
Query Match 31.1%; Score 19; DB 6; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 FMHNL 11
DB 4 FHTL 8

RESULT 3
ID 092766 PRELIMINARY; PRT; 9 AA.
AC 092766;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #5526/89;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
proximal coding part of the F gene of wild-type and vaccine distemper
morbilliviruses."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026237; AAC09167.1; -.
FT NON TER 9
FT SEQUENCE 9 AA; 1011 MW; F28173276053441 CRC64;
SQ
Query Match 31.1%; Score 19; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 10
DB 1 MHN 3

```

```

OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #10757/96;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
proximal coding part of the F gene of wild-type and vaccine distemper
morbilliviruses."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026234; AAC09164.1; -.
FT NON TER 9
FT SEQUENCE 9 AA; 1124 MW; F29D04576044041 CRC64;
SQ
Query Match 31.1%; Score 19; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 10
DB 1 MHN 3

RESULT 5
ID P82081 PRELIMINARY; PRT; 12 AA.
AC P82081;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DYNASTIN 3.
OS Limodynastes terraereginae (Northern banjo frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limodynastinae; Limodynastes.
OX NCBI_TaxID=104894;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=LIVER; GLAND.
RA Ratterly M.J., Bristford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
the banjo frogs Limodynastes terraereginae."
RL Limodynastes terraereginae."
RL Aust. J. Chem. 46:833-842(1993).
CC -1- MASS SPECTROMETRY: MW=1236; METHOD=PAB.
SQ SEQUENCE 12 AA; 1236 MW; 147AA70FDF472724 CRC64;

QY 8 MHN 12
DB 7 LNNLG 11

RESULT 6
ID 013591 PRELIMINARY; PRT; 8 AA.
AC 013591;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE ORF YNL337W (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Obermaler B., Piravandi E., Rinke M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]

```

RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z71612; CA96271.2; -  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 1005 MW; 5CA41E449C9C720 CRC64;

Query Match 29.5%; Score 18; DB 3; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FMEN 10  
 DB 4 FMEN 7

RESULT 7  
 ID Q8MES0 PRELIMINARY; PRT; 12 AA.  
 AC Q8MES0;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Ribosomal protein 16 (Fragment).  
 GN RPL16.  
 OS Anoda cristata.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Malvales; Malvaceae; Malvoideae; Anoda.  
 NCBI\_TaxID=183227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Peil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
 RT chloroplast DNA sequences of nchf and the rpl16 intron."  
 RL Syst. Bot. 27:333-350(2002).  
 DR EMBL: AF384567; AAM50405.1; -  
 DR GO: 0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1431 MW; 9A5E59B5452C9CA CRC64;

Query Match 29.5%; Score 18; DB 8; Length 12;  
 Best Local Similarity 37.5%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 EIOFMENL 11  
 DB 3 EPDFVNNI 10

RESULT 8  
 ID Q85631 PRELIMINARY; PRT; 12 AA.  
 AC Q85631;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE MH2, proviral DNA, myc to 3' LTR (Fragment).  
 OS Avian carcinoma virus.  
 OC Viruses; Retroviruses; Retroviridae; Alpharetrovirus.  
 NCBI\_TaxID=11958;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=85033920; PubMed=6092695;  
 RA Sutlive P., Jensen H.W., Bister K., Rapp U.R.;  
 RT "3'-terminal region of avian carcinoma virus MH2 shares sequence  
 RT elements with avian sarcoma viruses YJ3 and SR-A."  
 RL J. Virol. 52:703-705(1984).  
 DR EMBL: K03100; AAA42388.1; -  
 FT NON\_TER 1

SQ SEQUENCE 12 AA; 1466 MW; 72B4B884F30726DB CRC64;

Query Match 29.5%; Score 18; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNL 11  
 DB 2 HNL 4

RESULT 9  
 ID Q23876 PRELIMINARY; PRT; 11 AA.  
 AC Q23876;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE Actin 4.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
 NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=82260445; PubMed=6286214;  
 RA McKown M., Firtel R.A.;  
 RT "Actin multigene family of Dictyostelium."  
 RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).  
 DR EMBL: K02957; AAA33150.1; -  
 DR EMBL: K02956; AAA33150.1; JOINED.  
 SQ SEQUENCE 11 AA; 1205 MW; 72B54C46C6C2CAAB CRC64;

Query Match 27.9%; Score 17; DB 5; Length 11;  
 Best Local Similarity 28.6%; Pred. No. 1.6e+04;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 EIOFMEN 10  
 DB 5 DVQALNN 11

RESULT 10  
 ID P82085 PRELIMINARY; PRT; 12 AA.  
 AC P82085;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 7.  
 OS Limnodynastes salmiani (Salmian's-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 OC Limnodynastinae; Limnodynastes.  
 NCBI\_TaxID=39404;  
 RN [1]  
 RP SEQUENCE AND MASS SPECTROMETRY.  
 RA TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 RT Limnodynastes salmiani and Fletcherin from Limnodynastes fletcheri."  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -1- MASS SPECTROMETRY: MW=1114; METHOD=FAE.  
 SQ SEQUENCE 12 AA; 1114 MW; 3AB5A976CA7728 CRC64;

Query Match 27.9%; Score 17; DB 13; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+04;  
 Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 AVSEIOFMENL 12  
 DB 2 AVSGL-LTNLG 11

```

RESULT 11
Q28742 PRELIMINARY; PRT; 7 AA.
AC Q28742;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OC Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01598; AAA31415.1; -.
PIR; I46868; I46868.
FT NON TER 1
SQ SEQUENCE 7 AA; 916 MW; 681B1A1B69326B0 CRC64;

Query Match 26.2%; Score 16; DB 6; Length 7;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QFMEN 10
DB 1 QKMD 5

RESULT 12
Q05403 PRELIMINARY; PRT; 8 AA.
AC Q05403;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE DNA for ORF's from chromosome XV (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OC NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FY1679;
RX MEDLINE=96021609; PubMed=8533473;
RA Zumbstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RA "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames.";
RL Yeast 11:975-986(1995).
DR EMBL; X83121; CA58183.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E056 CRC64;

Query Match 26.2%; Score 16; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 11
DB 2 IHN 5

RESULT 13
Q40659 PRELIMINARY; PRT; 8 AA.
AC Q40659;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

```

```

DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Alpha-amylase (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriocaulaceae; Oryzaceae; Oryza.
OC NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91078641; PubMed=2258052;
RA Kumsang M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA Rodriguez R.L.;
RT "Expression and secretion of rice alpha-amylase by saccharomyces
RT cerevisiae.";
RL Gene 94:209-216(1990).
DR EMBL; M62916; AAA33892.1; -.
DR Gramene; Q40659; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;

Query Match 26.2%; Score 16; DB 10; Length 8;
Best Local Similarity 28.6%; Pred. No. 1e+06;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 IOFMEN 11
DB 1 NOVLNM 7

RESULT 14
P82082 PRELIMINARY; PRT; 8 AA.
AC P82082;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE DYNASTIN 4.
OS Limodysastes salmini (Salmin's-striped frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limodysastinae; Limodysastes.
OC NCBI_TaxID=39404;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT limodysastes salmini and Fletcherin from limodysastes fletcheri.";
RL Aust. J. Chem. 46:1235-1244(1993).
CC -1- MASS SPECTROMETRY; MW=772; METHOD=FAE.
SQ SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;

Query Match 26.2%; Score 16; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLG 12
DB 5 NLG 7

RESULT 15
P82083 PRELIMINARY; PRT; 8 AA.
AC P82083;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE DYNASTIN 5.
OS Limodysastes salmini (Salmin's-striped frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limodysastinae; Limodysastes.

```

OX NCBI\_TaxID=39404;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=SKIN SECRETION;  
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "Peptides from Australian frogs. The structure of the dynastins from  
Limodynastes salmini and Fletcheria from Limodynastes fletcheri.";  
RL Aust. J. Chem. 46:1235-1244(1993).  
CC -!- MASS SPECTROMETRY: MW=786; METHOD=PAD  
SQ SEQUENCE 8 AA; 786 MW; 7B58772455B05728 CRC64;  
  
Query Match 26.2%; Score 16; DB 13; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 10 NLG 12  
|||  
Db 5 NLG 7

Search completed: May 18, 2004, 10:04:48  
Job time : 30.25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: May 18, 2004, 09:42:39 ; Search time 45.75 seconds  
(without alignments)  
74.111 Million cell updates/sec

Title: US-09-730-174a-6  
Perfect score: 61  
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	50	82.0	11 6 ABG72607	Abg72607 Parathyro
2	50	82.0	12 6 ABG72608	Abg72608 Parathyro
3	49	80.3	11 3 AAY96968	Aay96968 Parathyro
4	42	68.9	10 2 AAB91644	Aab91644 Human par
5	42	68.9	10 3 AAY68767	Aay68767 Humano aci
6	42	68.9	10 4 AAB86219	Aab86219 Human par
7	42	68.9	10 6 ABR44166	AbR44166 Human par
8	41.5	68.0	11 2 AAY50600	Aay50600 Resin bou
9	41	67.2	9 4 AAB86225	Aab86225 Human par
10	39	63.9	9 3 AAB01862	Aab01862 PTH(1-14)
11	39	63.9	9 3 AAY96966	Aay96966 Parathyro
12	36	59.0	9 2 AAR91645	Aar91645 Human par
13	36	59.0	9 3 AAB01863	Aab01863 PTH(1-14)
14	36	59.0	9 3 AAY96981	Aay96981 Parathyro
15	36	59.0	9 4 AAB86220	Aab86220 Human par
16	36	59.0	10 4 AAB96932	Aab96932 Rat parat
17	36	59.0	11 4 AAB96931	Aab96931 Rat parat
18	36	59.0	11 4 AAB84770	Aab84770 Parathyro
19	36	59.0	11 4 AAB96915	Aab96915 Parathyro
20	36	59.0	12 4 AAB96914	Aab96914 Parathyro
21	36	59.0	12 4 AAB84769	Aab84769 Parathyro
22	34	55.7	12 2 AAW45785	Aaw45785 Parathyro
23	31	50.8	10 6 ABP71484	Abp71484 Parathyro
24	31	50.8	11 1 AAB82547	Aab82547 (Aen10, T
25	31	50.8	11 4 AAB96992	Aab96992 Rat parat

26	31	50.8	11 6 ABP71485	Abp71485 Parathyro
27	31	50.8	11 6 ABP71483	Abp71483 Parathyro
28	31	50.8	12 4 AAB96991	Aab96991 Rat parat
29	31	50.8	12 6 ABP71482	Abp71482 Parathyro
30	29	47.5	9 3 AAB01864	Aab01864 PTH(1-14)
31	29	47.5	9 3 AAY78849	Aay78849 Parathyro
32	29	47.5	9 3 AAY97062	Aay97062 PTH-rp N-
33	28	45.9	8 2 AAB91646	Aab91646 Human par
34	28	45.9	8 3 AAB07467	Aab07467 Human par
35	28	45.9	8 4 AAB86221	Aab86221 Antigenic
36	27	44.3	10 4 AAG63991	Aag63991 Human par
37	27	44.3	11 4 AAB54029	Aab54029 Complement
38	27	44.3	12 2 AAR50421	Aar50421 Human DNA
39	27	44.3	12 2 AAY55148	Aay55148 Antibody
40	27	44.3	12 3 AAY66894	Aay66894 Anti CD34
41	26	42.6	7 3 AAB00068	Aab00068 Human hae
42	26	42.6	9 3 AAB01866	Aab01866 N-termina
43	25	41.0	9 6 ABP83654	Abp83654 HLA prote
44	25	41.0	9 6 ABP89380	Abp89380 HLA prote
45	25	41.0	9 6 ABP88771	Abp88771 HLA prote

## ALIGNMENTS

RESULT 1	ABG72607	standard; peptide; 11 AA.
ID	ABG72607	
AC	ABG72607;	
XX		
DT	11-FEB-2003	(first entry)
XX		
DE	Parathyroid hormone antigenic peptide 2-12.	
XX		
KW	Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;	
KM	primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.	
XX		
OS	Homo sapiens.	
OS	Mus sp.	
OS	Rattus sp.	
OS	Bos taurus.	
OS	Sus scrofa.	
OS	Canis familiaris.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 6	/label= Leu, Phe
FT		
XX		
PN	US2002110871-A1.	
XX		
PD	15-AUG-2002.	
XX		
PF	05-DEC-2000; 2000US-00730174.	
XX		
PR	05-DEC-2000; 2000US-00730174.	
XX		
PA	(ZAHK/) ZAHKADNIK R J.	
XX	(LAVI/) LAVIGNE J R.	
PI	Zahradnik RJ, Lavigne JR;	
XX		
DR	WPI; 2003-06685/06.	
XX		
PT	New parathyroid hormone (PTH) antigenic peptide inducing the formation	
PT	and isolation of antibodies having an affinity to it, useful for	
PT	determining bioactive PTH levels in serum, plasma and/or cell culture	
XX	media.	
XX		
PS	Claim 1, Page 5, 11pp; English.	
XX		
CC	The invention relates to a new antigenic peptide for inducing the	
CC	formation and isolation of antibodies having an affinity to it, being	

CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
 CC are: (1) a method for producing antibodies useful in the determination of  
 CC PTH levels in a biological sample comprising: (a) providing at least one  
 CC first peptide antigen comprising a peptide fragment of PTH; (b)  
 CC administering the first peptide antigen to a host animal to induce  
 CC antibody production; (c) monitoring the antibody titre produced; (d)  
 CC isolating antisera produced in the host animal; and (e) selecting  
 CC antisera from the isolated antisera produced in the host that is capable  
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by  
 CC the method; and (3) test kits and analytical procedures used for the  
 CC determination of bioactive intact PTH utilising (ab). The method and  
 CC compositions of the present invention are useful for determining  
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
 CC The antigens, antibodies and methods of the present invention, as  
 CC compared to prior art, have the particular advantages of possessing  
 CC greater affinity for PTH, and in particular, are designed to have a novel  
 CC recognition for amino acid residues extending beyond the first N-terminal  
 CC PTH residue, and further have negligible cross-reactivity with the large  
 CC non-molecular forms of PTH. PTH levels are an important parameter in  
 CC patients suffering from hypercalcaemia, osteoporosis and primary  
 CC hyperparathyroidism. The present sequence represents a PTH antigenic  
 CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,  
 CC canine and bovine PTH  
 XX  
 SQ Sequence 11 AA;  
 Query Match 82.0%; Score 50; DB 6; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 2 VSEIQFMHNG 12  
 Db 1 VSEIQFMHNG 11  
 RESULT 2  
 ABG72608  
 ID ABG72608 standard; peptide; 12 AA.  
 XX  
 AC ABG72608;  
 XX  
 DT 11-FEB-2003 (first entry)  
 XX  
 DE Parathyroid hormone antigenic peptide 1-12.  
 XX  
 KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;  
 KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Rattus sp.  
 OS Bos taurus.  
 OS Sus scrofa.  
 OS Canis familiaris.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /label= Ser, Ala  
 FT Misc-difference 7 /label= Leu, Phe  
 FT  
 XX US2002110871-A1.  
 XX PN 15-AUG-2002.  
 XX PD 05-DEC-2000; 2000US-00730174.  
 XX PF 05-DEC-2000; 2000US-00730174.  
 XX PR 05-DEC-2000; 2000US-00730174.  
 XX PA (ZARR/) ZARRADNIK R J.  
 XX PA (LAVI/) LAVIGNE J R.  
 XX PI Zahradnik RJ, Lavigne JR;

XX  
 DR WPI; 2003-066685/06.  
 XX  
 PT New parathyroid hormone (PTH) antigenic peptide inducing the formation  
 PT and isolation of antibodies having an affinity to it, useful for  
 PT determining bioactive PTH levels in serum, plasma and/or cell culture  
 PT media.  
 XX  
 PS Claim 2; Page 5; 11pp; English.  
 XX  
 CC The invention relates to a new antigenic peptide for inducing the  
 CC formation and isolation of antibodies having an affinity to it, being  
 CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
 CC are: (1) a method for producing antibodies useful in the determination of  
 CC PTH levels in a biological sample comprising: (a) providing at least one  
 CC first peptide antigen comprising a peptide fragment of PTH; (b)  
 CC administering the first peptide antigen to a host animal to induce  
 CC antibody production; (c) monitoring the antibody titre produced; (d)  
 CC isolating antisera produced in the host animal; and (e) selecting  
 CC antisera from the isolated antisera produced in the host that is capable  
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by  
 CC the method; and (3) test kits and analytical procedures used for the  
 CC determination of bioactive intact PTH utilising (ab). The methods and  
 CC compositions of the present invention are useful for determining  
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
 CC The antigens, antibodies and methods of the present invention, as  
 CC compared to prior art, have the particular advantages of possessing  
 CC greater affinity for PTH, and in particular, are designed to have a novel  
 CC recognition for amino acid residues extending beyond the first N-terminal  
 CC PTH residue, and further have negligible cross-reactivity with the large  
 CC non-molecular forms of PTH. PTH levels are an important parameter in  
 CC patients suffering from hypercalcaemia, osteoporosis and primary  
 CC hyperparathyroidism. The present sequence represents a PTH antigenic  
 CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,  
 CC canine and bovine PTH  
 XX  
 SQ Sequence 12 AA;  
 Query Match 82.0%; Score 50; DB 6; Length 12;  
 Best Local Similarity 90.9%; Pred. No. 0.014;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 2 VSEIQFMHNG 12  
 Db 2 VSEIQFMHNG 12  
 RESULT 3  
 AAY96968  
 ID AAY96968 standard; peptide; 11 AA.  
 XX  
 AC AAY96968;  
 XX  
 DT 31-OCT-2000 (first entry)  
 XX  
 DE Parathyroid hormone N-terminal signaling domain (residues 1-11).  
 KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
 KW bone reformation; resorption; remodeling; tetrahel; osteoporosis.  
 XX  
 OS Homo sapiens.  
 OS  
 XX WO200039278-A2.  
 XX PN 06-JUL-2000.  
 XX PD 30-DEC-1999; 99WO-US031108.  
 XX PF 31-DEC-1998; 98US-0114577P.  
 XX PR 31-DEC-1998; 98US-0114577P.  
 XX PA (GARD/) GARDELLA T J.  
 XX PA (KRON/) KRONENBERG H M.  
 XX PA (POT/) POTTS J T.



PA (JUEP/) JUEPPNER H.  
XX  
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX WPI; 2000-452384/39.  
XX  
PT New compound comprising an amino terminal signaling functional domain  
PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
PT treating mammalian conditions characterized by decreases in bone mass.  
XX  
PS Claim 4; Page 92; 119pp; English.  
XX  
CC Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n  
CC -R are new. S is an amino terminal signaling functional domain of  
CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the  
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
CC sequence. The new compounds are used for treating mammalian conditions  
CC characterized by decreases in bone mass, determining rates of bone  
CC reformation, bone resorption and/or bone remodeling, treating diseases  
CC and disorders associated with decreased bone activity, increasing bone  
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHrp which avoids the need for  
CC regular injections to treat osteoporosis  
XX  
SQ Sequence 11 AA:  
Query Match 80.3%; Score 49; DB 3; Length 11;  
Best Local Similarity 90.9%; Pred. No. 0.02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AVSEIQFMHNL 11  
DB 1 AVSEIQFMHNL 11  
RESULT 4  
AAR91644  
ID AAR91644 standard; peptide; 10 AA.  
XX  
AC AAR91644;  
XX  
DT 06-NOV-1996 (first entry)  
XX  
DE Human parathyroid hormone antigenic peptide hPTH 1-10.  
XX  
KM Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
KM diagnosis; active hPTH 1-37.  
XX  
OS Synthetic.  
XX  
PN DE4434551-A1.  
XX  
PD 04-APR-1996.  
XX  
PF 28-SEP-1994; 94DE-04434551.  
XX  
PR 28-SEP-1994; 94DE-04434551.  
XX  
PA (FORSE/) FORSSMANN W.  
PI Adermann K, Forssmann W, Hock D, Meegerlein M;  
XX WPI; 1996-180391/19.  
XX  
PT New antigenic peptide(s) from human parathyroid hormone - and antibodies  
PT generated using them, able to distinguish between active and inactive  
PT forms of the hormone.  
XX  
PS Claim 2; Page 4; 5pp; German.  
XX

CC The present sequence is a specific example of claimed immunogenic  
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-  
CC terminal alpha-helical region and/or the non-structured region of the  
CC hormone. Antibodies and their binding fragments generated by injecting an  
CC animal with the peptides are useful as diagnostic reagents for  
CC determination of biologically active hPTH(1-37)  
XX  
SQ Sequence 10 AA:  
Query Match 68.3%; Score 42; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 0.37;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AVSEIQFMHNL 10  
DB 1 AVSEIQFMHNL 10  
RESULT 5  
AAY68767  
ID AAY68767 standard; peptide; 10 AA.  
XX  
AC AAY68767;  
XX  
DT 05-MAY-2000 (first entry)  
XX  
DE Amino acids 1-10 of a parathyroid hormone (PTH).  
XX  
KM Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;  
KM slimming treatment; cellulite; skin firming.  
XX  
OS Unidentified.  
XX  
PN WO200004047-A1.  
XX  
PD 27-JAN-2000.  
XX  
PF 07-JUL-1999; 99WO-FR001687.  
XX  
PR 17-JUL-1998; 98FR-00009193.  
XX  
PA (SEDE-) SEDERMA.  
XX  
PI Lintner K;  
XX  
DR WPI; 2000-171243/15.  
XX  
PT New parathyroid hormone fragment peptides, used as lipolysis stimulants  
PT in topically applied cosmetic compositions for slimming treatment of  
PT excessive weight in hips and thighs.  
XX  
PS Claim 1; Page 8; 16pp; French.  
XX  
CC The present sequence represents a parathyroid hormone (PTH) fragment,  
CC comprising amino acids 1-10. Parathyroid hormone fragments of the  
CC invention have lipolytic stimulating activity (especially when topically  
CC administered). The lipolytic activity of the peptides is enhanced when  
CC they are chemically modified to increase their lipophilicity. The  
CC peptides are used in cosmetic or dermatological compositions for skin  
CC care. They are especially used for slimming treatment of excessive weight  
CC in the thighs and hips, in the treatment of cellulite and for skin  
CC firming  
XX  
SQ Sequence 10 AA:  
Query Match 68.3%; Score 42; DB 3; Length 10;  
Best Local Similarity 80.0%; Pred. No. 0.37;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AVSEIQFMHNL 10  
DB 1 AVSEIQFMHNL 10

RESULT 6  
AAB86219 standard; peptide; 10 AA.  
XX  
AC AAB86219;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE Human parathyroid hormone immunogenic peptide SEQ ID 1.  
XX  
KM Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
KM diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
KM hypo-parathyroidism; hyper-parathyroidism.  
XX  
OS Homo sapiens.  
XX  
PN DE1961350-A1.  
XX  
PD 21-JUN-2001.  
XX  
PF 17-DEC-1999; 99DE-01061350.  
XX  
PR 17-DEC-1999; 99DE-01061350.  
XX  
PA (IMMU-) IMMUNDIAGNOSTIK AG.  
XX  
PI Armbruster FP;  
XX  
DR WPI; 2001-376318/40.  
XX  
PT Determining the content of physiologically active parathyroid hormone,  
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
PT reactive with different epitopes.  
XX  
PS Disclosure; Page 3; 10pp; German.  
XX  
CC This invention describes a novel method for determining (M1) the content  
CC of active parathyroid hormone (A) by treating a sample with (i) antibody  
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
CC and including the N-terminal residue and (ii) antibody (Ab2) that  
CC recognizes an epitope within the receptor-binding site of (A). The number  
CC of molecules that react with both antibodies is determined and used to  
CC calculate the content of physiologically active (A). The method is used  
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
CC active and (ii) that apparently intact peptide may be biologically  
CC inactive, and also takes into account the fact that some fragments of (A)  
CC are antagonistic (these have the receptor-binding site but lack the N-  
CC terminus). It thus provides a true measure of the content of active  
CC physiologically active (A); contrast methods that measure intact peptide  
CC and its 1-37 fragment which may produce falsely high values. This  
CC sequence represents a peptide fragment used to illustrate the method of  
CC the invention  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 68.9%; Score 42; DB 4; Length 10;  
Best Local Similarity 80.0%; Pred. No. 0.37;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DT 04-AUG-2003 (first entry)  
XX  
DE Human parathyroid hormone (hPTH) fragment (residues 1-10).  
XX  
KM Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;  
KM lipolysis; human; hPTH.  
XX  
OS Homo sapiens.  
XX  
PN WO2003035697-A1.  
XX  
PD 01-MAY-2003.  
XX  
PF 06-MAY-2002; 2002WO-KR00835.  
XX  
PR 27-SEP-2001; 2001KR-00060245.  
XX  
PR 15-MAR-2002; 2002KR-00014062.  
XX  
PA (GLDS ) LG HOUSEHOLD & HEALTH CARE LTD.  
XX  
PI Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H;  
PI Chang M;  
XX  
DR WPI; 2003-468288/44.  
XX  
PT Novel fusion peptide comprising self cell-penetrating Tat peptide bound  
PT to human parathyroid hormone-derived peptide, useful as component of skin  
PT slimming cosmetic composition.  
XX  
PS Claim 5; Page 6; 32pp; English.  
XX  
CC The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-  
CC penetrating Tat peptide is bound to human parathyroid hormone-derived  
CC peptide (hPTHDP). The fusion peptide is useful as a component of skin  
CC slimming cosmetic composition. The fusion peptide does not cause  
CC irritation, easily and safely penetrates into integument and endothelium,  
CC does not cause skin disease and has superior lipolysis effects, and is  
CC durable. The present sequence represents a human parathyroid hormone  
CC (hPTH) fragment that can be used to construct the fusion peptide  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 68.9%; Score 42; DB 6; Length 10;  
Best Local Similarity 80.0%; Pred. No. 0.37;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMEN 10  
:|||||  
DB 1 SVSEIQLMEN 10

RESULT 8  
AAY50600 standard; peptide; 11 AA.  
XX  
ID AAY50600  
XX  
AC AAY50600;  
XX  
DT 09-FEB-2000 (first entry)  
XX  
DE Resin bound cyclic peptide 33.  
XX  
KM Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;  
KM hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;  
KM osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;  
KM Cushing's syndrome; renal failure; hypertension; bone fracture repair.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "FMOC-Ala"  
FT FT  
FT Misc-difference 3 /note= "Ser(OcBu)"

```

FT  Misc-difference 4 /note= "Glu(OcBu)"
FT  Misc-difference 6 /note= "Gln(Trc)"
FT  Misc-difference 9 /note= "His(Trc)"
FT  Misc-difference 10 /note= "Asn(Trc)"
FT  Misc-difference 10 /note= "Asn(Trc)"
XX  WO9952933-A1.
XX  21-OCT-1999.
XX  15-APR-1999; 99WO-US008435.
XX  15-APR-1998; 98US-0081897P.
XX  (RHON ) RHONE-POULENC ROER PHARM INC.
XX  Sledeski AM, Mancel JJ;
XX  WPI; 1999-633822/54.
XX  Convergent synthesis of peptides for treating e.g. bone disorders.
XX  Disclosure; Page 75; 85pp; English.
XX  This invention describes a novel method for the preparation of peptides
XX  (II) that contain both cyclic and linear peptide fragments comprising
XX  sequential reaction of a resin-bound linear fragment with the cyclic
XX  fragment in N-protected form and optionally other linear fragments. The
XX  products of the invention have osteopathic and hypotensive activity. (II)
XX  bind to hPTH receptors and act as agonists or antagonists of hPTH. The
XX  method is particularly used to prepare cyclic peptide analogs of
XX  parathyroid hormone (PTH) or PTH-related peptides which are useful for
XX  treating diseases that respond to treatment with agents that bind to PTH
XX  receptors (with or without activation of adenyl cyclase activity), e.g.
XX  hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-
XX  parathyroidism, Cushing's syndrome, renal failure and hypertension, also
XX  for promoting repair of bone fractures. Separate synthesis of the cyclic
XX  fragment allows convergent synthesis of resin-bound (II), with better
XX  yields and higher throughput. The difficulties associated with
XX  preparation of the bridge fragment are confined to a small peptide which
XX  can be purified before reaction with the resin-bound component. AAY50568-
XX  Y50614 represent the peptide fragments described in the method of the
XX  invention
XX  Sequence 11 AA;
XX  SQ
XX  Query Match 68.0%; Score 41.5; DB 2; Length 11;
XX  Best Local Similarity 83.3%; Pred. No. 0.5;
XX  Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
XX  QY 1 AVSEIQFANLIG 12
XX  |||||:||||
XX  1 AVSEIQ-LHNLG 11
XX  DB
XX  RESULT 9
XX  ID AAB86225 standard; peptide; 9 AA.
XX  AAB86225;
XX  03-SEP-2001 (first entry)
XX  Human parathyroid hormone immunogenic peptide SEQ ID 7.
XX  Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
XX  diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
XX  hypo-parathyroidism; hyper-parathyroidism.
XX  Homo sapiens.
XX  OS

```

```

XX  DE19961350-A1.
XX  21-JUN-2001.
XX  17-DEC-1999; 99DE-01061350.
XX  17-DEC-1999; 99DE-01061350.
XX  (IMMU-) IMMUNDIAGNOSTIK AG.
XX  Armbruster FP;
XX  WPI; 2001-376318/40.
XX  Determining the content of physiologically active parathyroid hormone,
XX  useful in diagnosis of calcium-metabolism disorders, using two antibodies
XX  reactive with different epitopes.
XX  Disclosure; Page 3; 10pp; German.
XX  This invention describes a novel method for determining (M1) the content
XX  of active parathyroid hormone (A) by treating a sample with (i) antibody
XX  (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
XX  and including the N-terminal residue and (ii) antibody (Ab2) that
XX  recognizes an epitope within the receptor-binding site of (A). The number
XX  of molecules that react with both antibodies is determined and used to
XX  calculate the content of physiologically active (A). The method is used
XX  for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
XX  hyper-parathyroidism. The method (unlike known assays) recognizes that
XX  (i) some fragments of (A) shorter than the complete (84 aa) peptide are
XX  active and (ii) that apparently intact peptide may be biologically
XX  inactive, and also takes into account the fact that some fragments of (A)
XX  are antagonistic (these have the receptor-binding site but lack the N-
XX  terminus). It thus provides a true measure of the content of
XX  physiologically active (A); contrast methods that measure intact peptide
XX  and its 1-37 fragment which may produce falsely high values. This
XX  sequence represents a peptide fragment used to illustrate the method of
XX  the invention
XX  Sequence 9 AA;
XX  SQ
XX  Query Match 67.2%; Score 41; DB 4; Length 9;
XX  Best Local Similarity 88.9%; Pred. No. 1.4e+06;
XX  Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX  QY 2 VSEIQFPMN 10
XX  |||||:||||
XX  1 VSEIQFPMN 9
XX  DB
XX  RESULT 10
XX  ID AAB01862 standard; peptide; 9 AA.
XX  AAB01862;
XX  11-SEP-2000 (first entry)
XX  PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.
XX  Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
XX  calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
XX  bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX  Homo sapiens.
XX  Synthetic.
XX  WO200023594-A1.
XX  27-APR-2000.
XX  20-OCT-1999; 99WO-US024481.
XX  OS

```

XX 22-OCT-1998; 98US-0105530P.  
 XX (GARD/) GARDELLA T J.  
 XX (KRON/) KRONENBERG H M.  
 XX (POT/) POTTS J T.  
 XX (JUEP/) JUEPNER H.  
 XX Gardella TJ, Kronenberg HM, Potts JT, Juepner H;  
 XX WPI; 2000-339693/29.  
 XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
 XX acids that encode them, useful for treating osteoporosis.  
 XX Disclosure; Page 26; 73pp; English.  
 XX The invention relates to a novel parathyroid hormone (PTH) peptide  
 XX (AAB01859) and parathyroid hormone-related peptide (PTHrP, AAB01860), and  
 XX biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
 XX B01869). The peptides of the invention are at least 85% identical to the  
 XX generic peptide of the formula: X1-Val-Ser-Gln-X2-Gln-Leu-X3-His-X4-X5-  
 XX Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
 XX Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
 XX provided that the peptide is not PTHrP(1-14). The peptides of the  
 XX invention also encompass fragments of peptides of the invention  
 XX consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
 XX terminal derivatives. PTH is a major regulator of calcium homeostasis,  
 XX and is necessary for the normal function of the gastrointestinal,  
 XX skeletal, neurological system, neuromuscular and cardiovascular systems.  
 XX It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
 XX and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
 XX effect on the skeleton, and mediates calcium reabsorption, enhances  
 XX phosphate clearance and vitamin D synthesis in the kidney. A homologous  
 XX calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
 XX the renal and skeletal actions of PTH, and also bind to the PTH-1  
 XX receptor. They do not bind to the PTH-2 receptor. The peptides of the  
 XX invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
 XX AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
 XX B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
 XX conditions characterized by a decrease in bone mass, such as  
 XX osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
 XX medical disorders that arise from excessive or altered action of the PTH-  
 XX 1/PTH-2 receptor. Detectably labeled peptides of the invention are also  
 XX useful in the determination of rates of bone formation, bone resorption  
 XX and/or bone remodeling in a patient. The peptides of the invention are  
 XX "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
 XX conventional synthetic chemistry, and can be delivered to a patient via  
 XX non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
 XX PTH-1/PTH-2 receptor agonists  
 XX  
 XX Sequence 9 AA:  
 XX  
 XX Query Match 63.9%; Score 39; DB 3; Length 9;  
 XX Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 1 AVSEIQFMH 9  
 XX |||||  
 XX 1 AVSEIQLMH 9  
 XX  
 XX RESULT 11  
 XX ID AAY96966 standard; peptide; 9 AA.  
 XX AC AAY96966;  
 XX XX 31-OCT-2000 (first entry)  
 XX DT Parathyroid hormone N-terminal signaling domain (residues 1-9).  
 XX DE Parathyroid hormone; N-terminal, signaling domain; bone mass;  
 XX KM PTH; parathyroid hormone; N-terminal, signaling domain; bone mass;

KW bone reformation; resorption; remodeling; tether; osteoporosis.  
 XX  
 XX OS Homo sapiens.  
 XX XX WO200039278-A2.  
 XX XX 06-JUL-2000.  
 XX PD  
 XX PF 30-DEC-1999; 99WO-US031108.  
 XX XX 31-DEC-1998; 98US-0114577P.  
 XX (GARD/) GARDELLA T J.  
 XX (KRON/) KRONENBERG H M.  
 XX (POT/) POTTS J T.  
 XX (JUEP/) JUEPNER H.  
 XX Gardella TJ, Kronenberg HM, Potts JT, Juepner H;  
 XX WPI; 2000-452384/39.  
 XX New compound comprising an amino terminal signaling functional domain  
 XX linked to a carboxy-terminal binding portion of parathyroid hormone for  
 XX treating mammalian conditions characterized by decreases in bone mass.  
 XX Claim 4; Page 92; 119pp; English.  
 XX Compounds of the structure or formula S-(L)<sub>n</sub>-B, R<sub>1</sub>-S-(L)<sub>n</sub>-R or S-(L)<sub>n</sub>-  
 XX -R, are new. S is an amino terminal signaling functional domain of  
 XX parathyroid hormone (PTH); L is a linker molecule present n times (where  
 XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
 XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R<sub>1</sub> is the  
 XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
 XX sequence. The new compounds are used for treating mammalian conditions  
 XX characterized by decreases in bone mass, determining rates of bone  
 XX reformation, bone resorption and/or bone remodeling, treating diseases  
 XX and disorders associated with decreased tether activity, increasing cAMP  
 XX in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 XX non-peptide PTH (claimed). The new compound can be administered by  
 XX inhalation unlike the large native PTH or PTHrP which avoids the need for  
 XX regular injections to treat osteoporosis  
 XX  
 XX Sequence 9 AA:  
 XX  
 XX Query Match 63.9%; Score 39; DB 3; Length 9;  
 XX Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 1 AVSEIQFMH 9  
 XX |||||  
 XX 1 AVSEIQLMH 9  
 XX  
 XX RESULT 12  
 XX ID AAR91645 standard; peptide; 9 AA.  
 XX AC AAR91645;  
 XX XX 06-NOV-1996 (first entry)  
 XX DT Human parathyroid hormone antigenic peptide hPTH 1-9.  
 XX DE Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
 XX KM diagnosis; active hPTH 1-37.  
 XX OS Synthetic.  
 XX PN DE4434551-A1.  
 XX XX 04-APR-1996.  
 XX PD 28-SEP-1994; 94DE-04434551.  
 XX PF

[illegible]

CC	(AA01869) and parathyroid hormone-related peptide (PTHrP; AA01860), and CC biologically active derivatives thereof (AB01867-01868, AB01861-01869). The peptides of the invention are at least 85% identical to the glyceric peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-Gly-Lys-X6 (AB01867) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser; provided that the peptide is not PTHrP(1-14). The peptides of the invention also encompass fragments of peptides of the invention consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-terminal derivatives. PTH is a major regulator of calcium homeostasis, and is necessary for the normal function of the gastrointestinal, skeletal, neurological system, neuromuscular and cardiovascular systems. It binds to both PTH-1 receptors on osteoblasts and renal tubular cells, and to the recently identified PTH-2 receptor. PTH has a potent anabolic effect on the skeleton, and mediates calcium reabsorption, enhances phosphate clearance and vitamin D synthesis in the kidney. A homologous calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of the renal and skeletal actions of PTH, and also bind to the PTH-1 receptor. They do not bind to the PTH-2 receptor. The peptides of the invention are either agonists of PTH-1 and PTH-2 receptors (AA01858, AA01861-01866) or are PTH-1/PTH-2 receptor antagonists (AB01867-01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of conditions characterised by a decrease in bone mass, such as osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating medical disorders that arise from excessive or altered action of the PTH-1/PTH-2 receptor. Detectably labelled peptides of the invention are also useful in the determination of rates of bone formation, bone resorption and/or bone remodelling in a patient. The peptides of the invention are "minimised" versions of PTH or PTHrP which are inexpensive to prepare via conventional synthetic chemistry, and can be delivered to a patient via non-parenteral routes. Sequences AA01858 and AA01861-01866 represent PTH-1/PTH-2 receptor agonists
SO	Sequence 9 AA:
Query Match	59.0%; Score 36; DB 3; Length 9;
Best Local Similarity	77.8%; Pred. No. 1,4e+06;
Matches	7; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
Dc	1 AVSEIQFMH 9             1 AVSEIQLH 9
RESULT 14	
ID	AAV96981 standard; peptide; 9 AA. AAV96981
XX	AAV96981:
XX	
DT	31-OCT-2000 (first entry)
XX	
DE	Parathyroid hormone N-terminal signaling domain.
XX	
KW	PTH; parathyroid hormone; N-terminal; signaling domain; bone mass; bone remodelling; resorption; remodeling; tetherl; osteoporosis.
OS	Homo sapiens.
XX	
FN	WO200039278-A2.
PD	06-JUL-2000.
PF	30-DEC-1999; 99WO-US031108.
XX	
PR	31-DEC-1998; 98US-0114577P.
XX	
PA	(GARD/) GARDELIA T J.
PA	(KRON/) KROENBERG H M.
PA	(POTT/) POTTS J T.
PA	(JUEP/) JUEPPNER H.
XX	
JT	Gardelia TJ, Kroenbergh HM, Potts JT, Jueppner H,

XX DR WPI: 2000-452384/39.  
 XX  
 PT New compound comprising an amino terminal signaling functional domain  
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
 PT treating mammalian conditions characterized by decreases in bone mass.  
 XX  
 PS Claim 11; Page 33; 119pp; English.  
 CC  
 CC Compounds of the structure or formula S-(L)-n-R, R 1-S-(L)-n-R or S-(L)-n-  
 CC -R, are new. S is an amino terminal signaling functional domain of  
 CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
 CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
 CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the  
 CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
 CC sequence. The new compounds are used for treating mammalian conditions  
 CC characterized by decreases in bone mass, determining rates of bone  
 CC reformation, bone resorption and/or bone remodeling, treating diseases  
 CC and disorders associated with decreased bone activity, increasing cAMP  
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
 CC regular injections to treat osteoporosis  
 CC  
 SQ Sequence 9 AA;  
 QY  
 Db 1 AYSEIQFMH 9  
 1 SVSEIQLMH 9  
 Query Match 59.0%; Score 36; DB 3; Length 9;  
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 RESULT 15  
 AAB86220  
 ID AAB86220 standard; peptide; 9 AA.  
 AC AAB86220;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX  
 DE Human parathyroid hormone immunogenic peptide SEQ ID 2.  
 XX  
 KM Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
 KM diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
 KM hypo-parathyroidism; hyper-parathyroidism.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE19961350-A1.  
 XX  
 PD 21-JUN-2001.  
 XX  
 PF 17-DEC-1999; 99DE-01061350.  
 XX  
 PR 17-DEC-1999; 99DE-01061350.  
 XX  
 PA (IMMU-) IMMUNDIAGNOSTIK AG.  
 PI Armbruster FP;  
 DR WPI: 2001-376318/40.  
 XX  
 PT Determining the content of physiologically active parathyroid hormone,  
 PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
 PT reactive with different epitopes.  
 XX  
 PS Disclosure; Page 3; 10pp; German.  
 CC This invention describes a novel method for determining (M1) the content  
 CC of active parathyroid hormone (A) by treating a sample with (1) antibody

CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
 CC and including the N-terminal residue and (1) antibody (Ab2) that  
 CC recognizes an epitope within the receptor-binding site of (A). The number  
 CC of molecules that react with both antibodies is determined and used to  
 CC calculate the content of physiologically active (A). The method is used  
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
 CC (1) some fragments of (A) shorter than the complete (84 aa) peptide are  
 CC active and (1) that apparently intact peptide may be biologically  
 CC inactive, and also takes into account the fact that some fragments of (A)  
 CC are antagonistic (these have the receptor-binding site but lack the N-  
 CC terminus). It thus provides a true measure of the content of  
 CC physiologically active (A); contrast methods that measure intact peptide  
 CC and its 1-37 fragment which may produce falsely high values. This  
 CC sequence represents a peptide fragment used to illustrate the method of  
 CC the invention  
 CC  
 SQ Sequence 9 AA;  
 QY  
 Db 1 AYSEIQFMH 9  
 1 SVSEIQLMH 9  
 Query Match 59.0%; Score 36; DB 4; Length 9;  
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Search completed: May 18, 2004, 10:01:54  
 Job time : 45.75 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: May 18, 2004, 10:04:51 ; Search time 33.25 Seconds

(Without alignments)  
100.425 Million cell updates/sec

Title: US-09-730-174A-6

Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 166097

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10C\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	61	100.0	12 9 US-09-730-174A-6	Sequence 6, Appl1
2	58	95.1	12 9 US-09-730-174A-4	Sequence 4, Appl1
3	57	93.4	11 9 US-09-730-174A-2	Sequence 2, Appl1
4	55	90.2	12 9 US-09-730-174A-5	Sequence 5, Appl1
5	52	85.2	12 9 US-09-730-174A-3	Sequence 3, Appl1
6	51	83.6	11 9 US-09-730-174A-1	Sequence 1, Appl1
7	42	68.9	10 14 US-10-168-185-1	Sequence 7, Appl1
8	41	67.2	9 14 US-10-168-185-7	Sequence 1, Appl1
9	39	63.9	9 14 US-10-192-673-6	Sequence 6, Appl1
10	37	60.7	8 14 US-10-168-185-8	Sequence 8, Appl1
11	36	59.0	9 14 US-10-192-673-7	Sequence 7, Appl1
12	36	59.0	9 14 US-10-168-185-2	Sequence 2, Appl1
13	29	47.5	9 14 US-10-192-673-8	Sequence 8, Appl1
14	28	45.9	8 14 US-10-168-185-3	Sequence 3, Appl1
15	27	44.3	10 14 US-10-232-187-8	Sequence 8, Appl1

16	27	44.3	10 15 US-10-366-709-2	Sequence 2, Appl1
17	26	42.6	9 14 US-10-192-673-10	Sequence 10, Appl1
18	25	41.0	10 9 US-09-976-787-4	Sequence 4, Appl1
19	25	41.0	10 9 US-09-865-198-4	Sequence 4, Appl1
20	25	41.0	10 9 US-09-965-099-12	Sequence 12, Appl1
21	25	41.0	10 10 US-09-563-222-41	Sequence 41, Appl1
22	25	41.0	10 10 US-09-798-689-4	Sequence 4, Appl1
23	25	41.0	10 10 US-10-239-656-19	Sequence 19, Appl1
24	25	41.0	10 13 US-10-051-852-12	Sequence 12, Appl1
25	25	41.0	10 14 US-10-195-752-108	Sequence 108, Appl1
26	25	41.0	10 14 US-10-160-232-12	Sequence 12, Appl1
27	25	41.0	10 14 US-10-160-232-18	Sequence 18, Appl1
28	25	41.0	10 14 US-10-283-349-49	Sequence 49, Appl1
29	25	41.0	10 14 US-10-230-880-115	Sequence 115, Appl1
30	25	41.0	10 15 US-10-137-867-526	Sequence 526, Appl1
31	25	41.0	10 15 US-10-366-709-3	Sequence 3, Appl1
32	25	41.0	10 15 US-10-430-176-12	Sequence 12, Appl1
33	25	41.0	11 11 US-09-791-551-13	Sequence 13, Appl1
34	24	39.3	9 9 US-09-834-765-45	Sequence 45, Appl1
35	24	39.3	9 9 US-09-834-765-55	Sequence 55, Appl1
36	24	39.3	10 9 US-09-834-765-73	Sequence 73, Appl1
37	24	39.3	10 9 US-09-834-765-78	Sequence 78, Appl1
38	24	39.3	10 9 US-09-910-059-26	Sequence 26, Appl1
39	24	39.3	10 14 US-10-033-741-61	Sequence 61, Appl1
40	24	39.3	11 14 US-10-153-334-14	Sequence 14, Appl1
41	24	39.3	12 14 US-10-319-130-16	Sequence 16, Appl1
42	23	37.7	6 14 US-10-168-185-5	Sequence 5, Appl1
43	23	37.7	7 14 US-10-168-185-4	Sequence 4, Appl1
44	23	37.7	8 14 US-10-043-487-508	Sequence 508, Appl1
45	23	37.7	9 14 US-10-147-140-26	Sequence 26, Appl1

## ALIGNMENTS

RESULT 1  
US-09-730-174A-6  
Sequence 6, Application US/09730174A  
Patent No. US20020110871A1  
GENERAL INFORMATION:  
APPLICANT: Zahradnik, R.J.  
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Hc  
FILE REFERENCE: IMUNE-001A  
CURRENT APPLICATION NUMBER: US/09/730.174A  
CURRENT FILING DATE: 2000-12-05  
NUMBER OF SEQ ID NOS: 12  
SEQ ID NO 6  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
US-09-730-174A-6

Query Match 100.0%; Score 61; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AVSEIQFMHNLG 12  
Db 1 AVSEIQFMHNLG 12

RESULT 2  
US-09-730-174A-4  
Sequence 4, Application US/09730174A  
Patent No. US20020110871A1  
GENERAL INFORMATION:  
APPLICANT: Zahradnik, R.J.  
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Hc  
FILE REFERENCE: IMUNE-001A

```

; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4

Query Match
Best Local Similarity 95.1%; Score 58; DB 9; Length 12;
Pred. No. 0.00043;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQFMHNLG 12
Db 1 SVSEIQFMHNLG 12

RESULT 3
US-09-730-174A-2
; Sequence 2, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMNE-001A
; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-2

Query Match
Best Local Similarity 93.4%; Score 57; DB 9; Length 11;
Pred. No. 0.0006;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQFMHNLG 12
Db 1 VSEIQFMHNLG 11

RESULT 4
US-09-730-174A-5
; Sequence 5, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMNE-001A
; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5

Query Match
Best Local Similarity 90.2%; Score 55; DB 9; Length 12;
Pred. No. 0.0015;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 AVSEIQFMHNLG 12
Db 1 AVSEIQFMHNLG 12

RESULT 5
US-09-730-174A-3
; Sequence 3, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMNE-001A
; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3

Query Match
Best Local Similarity 85.2%; Score 52; DB 9; Length 12;
Pred. No. 0.0055;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMHNLG 12
Db 1 SVSEIQFMHNLG 12

RESULT 6
US-09-730-174A-1
; Sequence 1, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMNE-001A
; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1

Query Match
Best Local Similarity 83.6%; Score 51; DB 9; Length 11;
Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQFMHNLG 12
Db 1 VSEIQFMHNLG 11

RESULT 7
US-10-166-185-1
; Sequence 1, Application US/10166185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Miesbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
```



FILE REFERENCE: HLZ-004US  
CURRENT APPLICATION NUMBER: US/10/168,185  
CURRENT FILING DATE: 2002-06-17  
PRIOR APPLICATION NUMBER: PCT/EP00/12911  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: DE 19961350  
PRIOR FILING DATE: 1999-12-17  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-168-185-1

Query Match 68.3%; Score 42; DB 14; Length 10;  
Best Local Similarity 80.0%; Pred. No. 0.33;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 10  
DB 1 VSEIQLMH 10

## RESULT 8

US-10-168-185-7  
Sequence 7, Application US/10168185  
Publication No. US20030175802A1  
GENERAL INFORMATION:  
APPLICANT: Armbruster, Franz Paul  
APPLICANT: Mischler, Albert  
APPLICANT: Schmidt-Gayk, Heinrich  
APPLICANT: Roth, Heinz-Jürgen  
TITLE OF INVENTION: Method for Determining Parathormone  
FILE REFERENCE: HLZ-004US  
CURRENT APPLICATION NUMBER: US/10/168,185  
CURRENT FILING DATE: 2002-06-17  
PRIOR APPLICATION NUMBER: PCT/EP00/12911  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: DE 19961350  
PRIOR FILING DATE: 1999-12-17  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-168-185-7

Query Match 67.2%; Score 41; DB 14; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1e+06;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQFMH 10  
DB 1 VSEIQLMH 9

## RESULT 9

US-10-192-673-6  
Sequence 6, Application US/10192673  
Publication No. US2003016838A1  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)  
FILE REFERENCE: 0609.4570002

CURRENT APPLICATION NUMBER: US/10/192,673  
CURRENT FILING DATE: 2002-07-11  
PRIOR APPLICATION NUMBER: U.S. 09/421,379  
PRIOR FILING DATE: 1999-10-20  
PRIOR APPLICATION NUMBER: U.S. 60/105,530  
PRIOR FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-192-673-6

Query Match 63.9%; Score 39; DB 14; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1e+06;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9  
DB 1 AVSEIQLMH 9

## RESULT 10

US-10-168-185-8  
Sequence 8, Application US/10168185  
Publication No. US20030175802A1  
GENERAL INFORMATION:  
APPLICANT: Armbruster, Franz Paul  
APPLICANT: Mischler, Albert  
APPLICANT: Schmidt-Gayk, Heinrich  
APPLICANT: Roth, Heinz-Jürgen  
TITLE OF INVENTION: Method for Determining Parathormone  
FILE REFERENCE: HLZ-004US  
CURRENT APPLICATION NUMBER: US/10/168,185  
CURRENT FILING DATE: 2002-06-17  
PRIOR APPLICATION NUMBER: PCT/EP00/12911  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: DE 19961350  
PRIOR FILING DATE: 1999-12-17  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-168-185-8

Query Match 60.7%; Score 37; DB 14; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SEIQFMH 10  
DB 1 SEIQLMH 8

## RESULT 11

US-10-192-673-7  
Sequence 7, Application US/10192673  
Publication No. US2003016838A1  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)

```
FILE REFERENCE: 0609.4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-10-192-673-7
```

```
Query Match          59.0%; Score 36; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 AVSEIQPMH 9
   |||||
Db 1 AVSEIQLMH 9
```

## RESULT 12

```
US-10-168-185-2
Sequence 2, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jürgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-185-2
```

```
Query Match          59.0%; Score 36; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 AVSEIQPMH 9
   |||||
Db 1 SVSEIQLMH 9
```

## RESULT 13

```
US-10-192-673-8
Sequence 8, Application US/10192673
Publication No. US2003016838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
Parathyroid Hormone (PTH) and Parathyroid
```

```
TITLE OF INVENTION: Hormone-Related Peptide (PTH-P)
FILE REFERENCE: 0609.4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-10-192-673-8
```

```
Query Match          47.5%; Score 29; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AVSEIQPMH 9
   |||||
Db 1 AVSEHQLMH 9
```

## RESULT 14

```
US-10-168-185-3
Sequence 3, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jürgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-185-3
```

```
Query Match          45.3%; Score 28; DB 14; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 AVSEIQPMH 8
   |||||
Db 1 SVSEIQLMH 8
```

## RESULT 15

```
US-10-232-187-8
Sequence 8, Application US/10232187
Publication No. US20030092091A1
GENERAL INFORMATION:
APPLICANT: Abrahamson, Julie A.
APPLICANT: Bochner, Bruce
APPLICANT: Erickson-Miller, Connie L.
APPLICANT: Kikly, Kristine K.
APPLICANT: Schleimer, Robert
```

Tue May 18 12:03:11 2004

us-09-730-174a-6.closed.rapb

Page 5

APPLICANT: Nulku, Turkan E.  
TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies  
FILE REFERENCE: GH50042-1  
CURRENT APPLICATION NUMBER: US/10/232,187  
CURRENT FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: 60/187,595  
PRIOR FILING DATE: 2000-03-07  
PRIOR APPLICATION NUMBER: PCT/US01/07193  
PRIOR FILING DATE: 2001-03-05  
PRIOR APPLICATION NUMBER: 60/315,943  
PRIOR FILING DATE: 2001-08-30  
PRIOR APPLICATION NUMBER: 60/349,830  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: 60/394,741  
PRIOR FILING DATE: 2002-07-10  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-232-187-8

Query Match 44.3%; Score 27; DB 14; Length 10;  
Best Local Similarity 44.4%; Pred. No. 2e+02; 3; Indels 0; Gaps 0;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIOFMH 9  
| : : |  
Db 2 ATSSVSVMH 10

Search completed: May 18, 2004, 10:21:00  
Job time : 33.25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

CM protein - protein search, using sw model

Run on: May 18, 2004, 09:58:45 ; Search time 12.75 Seconds  
(without alignments)  
48,589 Million cell updates/sec

Title: US-09-730-174a-6  
Perfect score: 61  
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	49	80.3	12 4 US-09-442-989-31	Sequence 31, Appl
2	42	68.9	10 3 US-08-817-547A-1	Sequence 1, Appl
3	39	63.9	9 4 US-09-421-379-6	Sequence 6, Appl
4	36	59.0	9 3 US-08-817-547A-2	Sequence 2, Appl
5	31	50.8	9 4 US-09-421-379-7	Sequence 7, Appl
6	31	50.8	11 6 5460978-3	Patent No. 5460978
7	29	47.5	9 4 US-09-421-379-8	Sequence 8, Appl
8	29	47.5	12 2 US-08-140-137A-42	Sequence 42, Appl
9	28	45.9	8 3 US-08-817-547A-3	Sequence 3, Appl
10	27	44.3	12 2 US-08-482-228-42	Sequence 42, Appl
11	27	44.3	12 3 US-08-482-528-42	Sequence 42, Appl
12	26	42.6	9 4 US-09-421-379-10	Sequence 10, Appl
13	25	41.0	10 2 US-08-116-778E-9	Sequence 9, Appl
14	25	41.0	10 2 US-08-438-562-9	Sequence 9, Appl
15	25	41.0	10 2 US-08-483-528B-97	Sequence 97, Appl
16	25	41.0	10 3 US-08-783-853A-12	Sequence 49, Appl
17	25	41.0	10 3 US-08-836-561-49	Sequence 12, Appl
18	25	41.0	10 3 US-09-280-028-12	Sequence 12, Appl
19	25	41.0	10 4 US-09-344-050-12	Sequence 12, Appl
20	25	41.0	10 4 US-09-393-385B-108	Sequence 108, Appl
21	25	41.0	10 4 US-09-434-122-49	Sequence 49, Appl
22	25	41.0	10 4 US-09-091-071-3	Sequence 3, Appl
23	24	39.3	5 2 US-08-177-109A-56	Sequence 56, Appl
24	24	39.3	5 3 US-08-687-706-56	Sequence 56, Appl
25	24	39.3	5 3 US-08-817-547A-17	Sequence 17, Appl
26	24	39.3	6 3 US-08-817-547A-16	Sequence 16, Appl
27	24	39.3	7 3 US-08-817-547A-15	Sequence 15, Appl

28	24	39.3	8 2 US-08-748-021-64	Sequence 64, Appl
29	24	39.3	8 3 US-08-817-547A-14	Sequence 14, Appl
30	24	39.3	8 3 US-08-974-297-64	Sequence 64, Appl
31	24	39.3	9 3 US-08-817-547A-13	Sequence 13, Appl
32	24	39.3	10 3 US-08-432-694-5	Sequence 5, Appl
33	24	39.3	10 3 US-08-817-547A-7	Sequence 7, Appl
34	24	39.3	10 3 US-09-171-945-26	Sequence 26, Appl
35	24	39.3	11 1 US-08-432-694-3	Sequence 3, Appl
36	23	37.7	6 3 US-08-817-547A-5	Sequence 5, Appl
37	23	37.7	7 3 US-08-817-547A-4	Sequence 4, Appl
38	23	37.7	9 1 US-07-822-043-26	Sequence 26, Appl
39	23	37.7	9 1 US-08-346-455B-26	Sequence 26, Appl
40	23	37.7	9 3 US-08-977-221-26	Sequence 26, Appl
41	23	37.7	9 4 US-09-483-831B-26	Sequence 26, Appl
42	23	37.7	9 5 PCT-US95-06613-26	Sequence 26, Appl
43	23	37.7	10 4 US-09-771-415-3	Sequence 3, Appl
44	23	37.7	12 3 US-09-064-750-1	Sequence 1, Appl
45	22	36.1	10 1 US-08-615-181-83	Sequence 83, Appl

## ALIGNMENTS

RESULT 1  
US-09-442-989-31  
Sequence 31, Application US/09442989  
Patent No. 6569993  
GENERAL INFORMATION:  
APPLICANT: Siedeski, Adam W.  
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC  
FILE REFERENCE: A3113B-US  
CURRENT APPLICATION NUMBER: US/09/442,989  
EARLIER FILING DATE: 1993-11-18  
EARLIER APPLICATION NUMBER: 60/081,897  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 31  
LENGTH: 12  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)  
OTHER INFORMATION: FMOC-Ala  
NAME/KEY: PEPTIDE  
LOCATION: (3)  
OTHER INFORMATION: Ser(OtBu)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (4)  
OTHER INFORMATION: Glu(OtBu)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (6)  
OTHER INFORMATION: Glu(Trt)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (9)  
OTHER INFORMATION: His(Trt)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (10)  
OTHER INFORMATION: Asn(Trt)  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (8)  
OTHER INFORMATION: Nle  
US-09-442-989-31

Query Match 80.3%; Score 49; DB 4; Length 12;  
Best Local Similarity 83.3%; Pred. No. 0.0034;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIOFMNLG 12  
Db 1 AVSEIOQLXNHLG 12

RESULT 2  
US-08-817-547A-1  
; Sequence 1, Application US/08817547A  
; Patent No. 6030790  
; GENERAL INFORMATION:  
; APPLICANT: Ademann, Knut  
; APPLICANT: Hock, Dieter  
; APPLICANT: Magerlein, Markus  
; TITLE OF INVENTION: Peptides from the hPTH Sequence  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew, LLP  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,547A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/03757  
; FILING DATE: 29 SEPT 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FROST, ROGER T.  
; REGISTRATION NUMBER: 22,176  
; REFERENCE/DOCKET NUMBER: 07826-0007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-818-3700  
; TELEFAX: 404-818-3799  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: no  
; ANTI-SENSE: no  
US-08-817-547A-1

Query Match 68.9%; Score 42; DB 3; Length 10;  
Best Local Similarity 80.0%; Pred. No. 0.06;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIOFMHN 10  
Db 1 SVSEIOQLMHN 10

RESULT 3  
US-09-421-379-6  
; Sequence 6, Application US/09421379  
; Patent No. 6495662  
; GENERAL INFORMATION:  
; APPLICANT: Gardella, Thomas J.  
; APPLICANT: Kironenbery, Henry  
; APPLICANT: Potts, John T.  
; APPLICANT: Juppner, Harald

TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
; FILE REFERENCE: 0609.4570001  
; CURRENT APPLICATION NUMBER: US/09/421,379  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: U.S. 60/105,530  
; EARLIER FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-421-379-6

Query Match 63.9%; Score 39; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIOFMH 9  
Db 1 AVSEIOQLMH 9

RESULT 4  
US-08-817-547A-2  
; Sequence 2, Application US/08817547A  
; Patent No. 6030790  
; GENERAL INFORMATION:  
; APPLICANT: Ademann, Knut  
; APPLICANT: Hock, Dieter  
; APPLICANT: Magerlein, Markus  
; TITLE OF INVENTION: Peptides from the hPTH Sequence  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew, LLP  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,547A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/03757  
; FILING DATE: 29 SEPT 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FROST, ROGER T.  
; REGISTRATION NUMBER: 22,176  
; REFERENCE/DOCKET NUMBER: 07826-0007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-818-3700  
; TELEFAX: 404-818-3799  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: no  
; ANTI-SENSE: no  
US-08-817-547A-2

Query Match 59.0%; Score 36; DB 3; Length 9;  
Best Local Similarity 77.8%; Pred. No. 3e+05;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9  
Db 1 AVSEIQLMH 9

RESULT 5  
US-09-421-379-7  
Sequence 7, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)  
FILE REFERENCE: 0609.4570001  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-421-379-7

Query Match 59.0%; Score 36; DB 4; Length 9;  
Best Local Similarity 77.8%; Pred. No. 3e+05;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9  
Db 1 AVSEIQLMH 9

RESULT 6  
5460978-3  
Patent No. 5460978  
APPLICANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,  
; BRUCE E.; WETTENHALL, RICHARD E.H.  
TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL  
; HYPERCALCEMIA OF MALIGNANCY-PTHrP  
NUMBER OF SEQUENCES: 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/715,280  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 199,235  
FILING DATE: 09-MAY-1988  
APPLICATION NUMBER:  
FILING DATE:  
SEQ ID NO:3  
LENGTH: 11  
5460978-3

Query Match 50.8%; Score 31; DB 6; Length 11;  
Best Local Similarity 70.0%; Pred. No. 8.5;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 10

Db 1 AVSEHQLMH 10

RESULT 7  
US-09-421-379-8  
Sequence 8, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)  
FILE REFERENCE: 0609.4570001  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-421-379-8

Query Match 47.5%; Score 29; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9  
Db 1 AVSEHQLMH 9

RESULT 8  
US-08-140-137A-42  
Sequence 42, Application US/08140137A  
Patent No. 5817617  
GENERAL INFORMATION:  
APPLICANT: TUOMANEN, ELAINE  
APPLICANT: MASURE, H. R.  
TITLE OF INVENTION: ANALOGS OF ENDOTHELIAL LEUKOCYTE  
TITLE OF INVENTION: ADHESION MOLECULE (ELAM)  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/140,137A  
FILING DATE: 27-MAY-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-096  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684

TELEX: 133521  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
DESCRIPTION: Card peptide sequence  
US-08-140-137A-42

Query Match 47.5%; Score 29; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 22;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQFMH 9  
DB 5 ISEIQFVH 12

RESULT 9  
US-08-817-547A-3  
Sequence 3, Application US/08817547A  
Patent No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Adermann, Knut  
APPLICANT: Hock, Dieter  
TITLE OF INVENTION: Peptides from the hPTH Sequence  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
City: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHEICAL: no  
ANTI-SENSE: no  
US-08-817-547A-3

Query Match 45.9%; Score 28; DB 3; Length 8;  
Best Local Similarity 75.0%; Pred. No. 3e+05;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 8  
DB 1 SVSEIQFMH 8

RESULT 10  
US-08-482-228-42  
Sequence 42, Application US/08482228  
Patent No. 5968753  
GENERAL INFORMATION:  
APPLICANT: Tseng-Law, Janet  
APPLICANT: Kobori, Joan A.  
APPLICANT: Al-Abdaly, Fahad A.  
APPLICANT: Guillermo, Roy  
APPLICANT: Helgeson, Sam L.  
APPLICANT: Deans, Robert J.  
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL  
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE  
NUMBER OF SEQUENCES: 215  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janice Guthrie, Ph.D.  
STREET: P.O. Box 15210  
City: Irvine  
STATE: California  
COUNTRY: USA  
ZIP: 92713-5210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,228  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Guthrie, Janice  
REGISTRATION NUMBER: 35,170  
REFERENCE/DOCKET NUMBER: IT-4630CIP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 440-5353  
TELEFAX: (714) 553-1952  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-228-42

Query Match 44.3%; Score 27; DB 2; Length 12;  
Best Local Similarity 55.6%; Pred. No. 54;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9  
DB 3 ASSSVTFMH 11

RESULT 11  
US-08-482-528-42  
Sequence 42, Application US/08482528  
Patent No. 6017719  
GENERAL INFORMATION:  
APPLICANT: Tseng-Law, Janet  
APPLICANT: Kobori, Joan A.  
APPLICANT: Al-Abdaly, Fahad A.  
APPLICANT: Guillermo, Roy  
APPLICANT: Helgeson, Sam L.  
APPLICANT: Deans, Robert J.  
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL  
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE  
NUMBER OF SEQUENCES: 215  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janice Guthrie, Ph.D.  
STREET: P.O. Box 15210  
City: Irvine

STATE: California  
COUNTRY: USA  
ZIP: 92713-5210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,528  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Guthe, Janice  
REGISTRATION NUMBER: 35,170  
REFERENCE/DOCKET NUMBER: IT-4630CIP4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 440-5353  
TELEFAX: (714) 553-1952  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-528-42

Query Match 44.3%; Score 27; DB 3; Length 12;  
Best Local Similarity 55.6%; Pred. No. 54;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIQPMH 9  
DB 3 ASSSVTFMH 11

RESULT 12  
US-09-421-379-10  
Sequence 10, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)  
FILE REFERENCE: 0609.4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 10  
LENGTH: 9  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: peptide  
US-09-421-379-10

Query Match 42.6%; Score 26; DB 4; Length 9;  
Best Local Similarity 55.6%; Pred. No. 3e+05;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIQPMH 9  
DB 1 SVSEHQLH 9

RESULT 13  
US-08-116-778E-9  
Sequence 9, Application US/08116778E  
Patent No. 5830470  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KIWANA, YOSHIOHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/116,778E  
FILING DATE: 07-SEP-93  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 243-59  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-116-778E-9

Query Match 41.0%; Score 25; DB 2; Length 10;  
Best Local Similarity 44.4%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIQPMH 9  
DB 2 ASSSVTFMH 10

RESULT 14  
US-08-438-562-9  
Sequence 9, Application US/08438562  
Patent No. 5874255  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KIWANA, YOSHIOHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/06/438,562  
FILING DATE: 10-MAY-95  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/116,778  
FILING DATE: 07-SEP-93  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY T.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 249-76  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-438-562-9

Query Match 41.0%; Score 25; DB 2; Length 10;  
Best Local Similarity 44.4%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIOFMH 9  
Db 2 ASSSVSYMH 10

RESULT 15  
US-08-483-5288-97  
Sequence 97, Application US/084835288  
Patent No. 5939532  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUMANA, YOSHIIISA  
APPLICANT: HASEGAWA, NAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/06/483,528B  
FILING DATE: 07-JUN-95  
CLASSIFICATION: 536  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 97:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-483-5288-97

Query Match 41.0%; Score 25; DB 2; Length 10;  
Best Local Similarity 44.4%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIOFMH 9  
Db 2 ASSSVSYMH 10

Search completed: May 18, 2004, 10:06:44  
Job time : 12.75 secs